

FIG. 1A

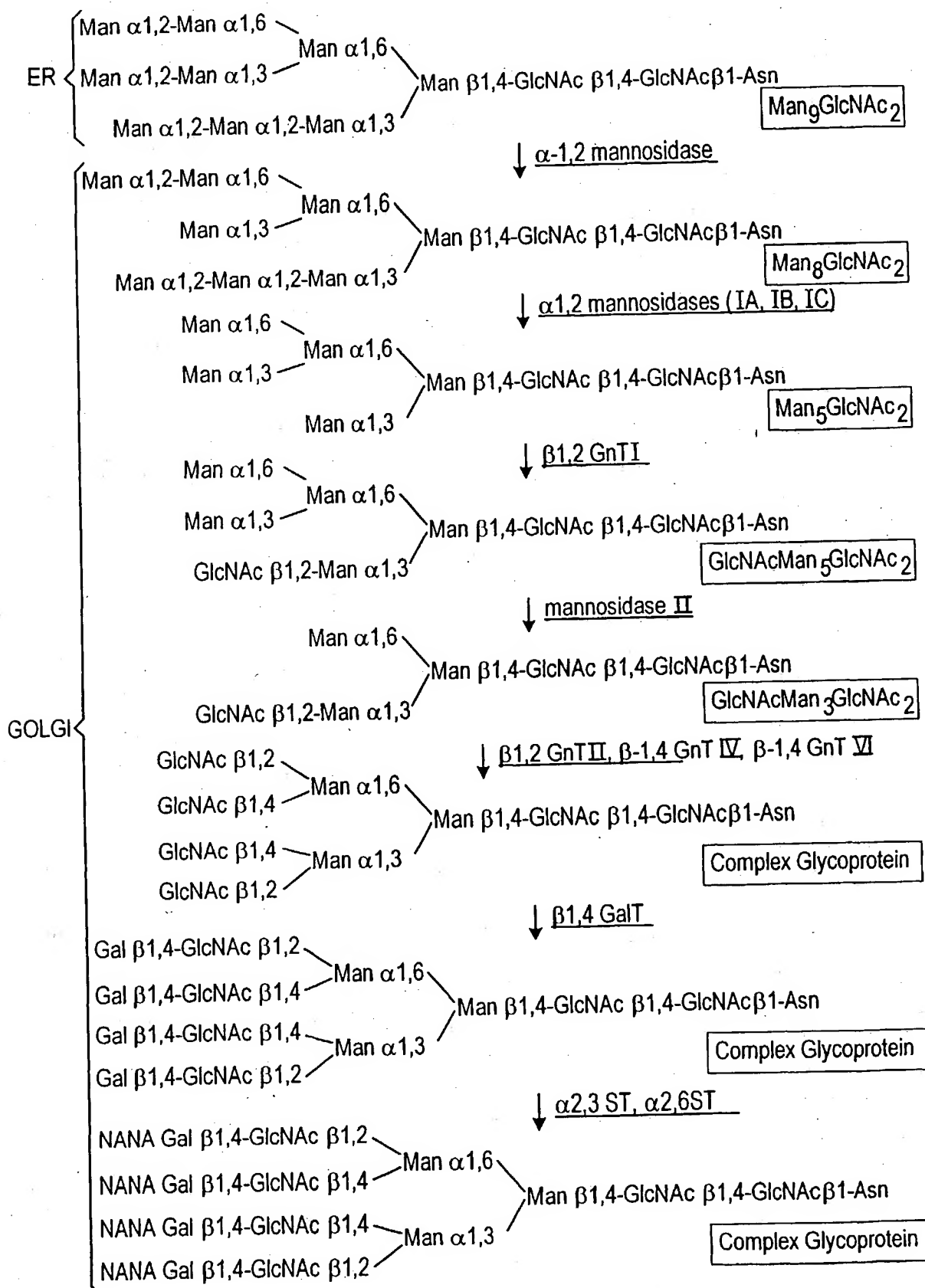


FIG. 1B

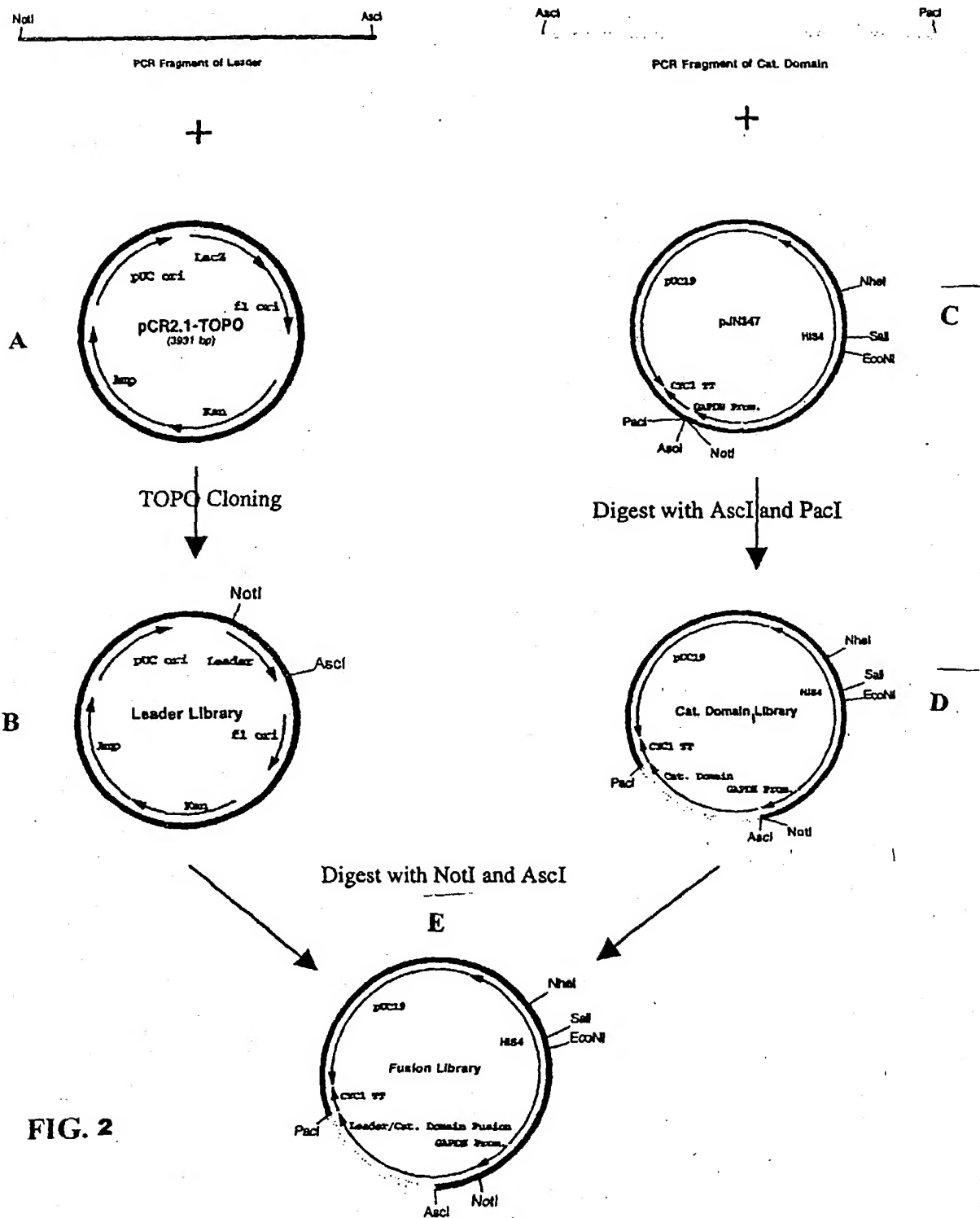


FIG. 2

**FIG. 3**

**M. musculus alpha-1,2-mannosidase IA open reading frame.** The transmembrane and catalytic domains are highlighted in bold respectively. The sequence of the primers used to generate the N-terminal truncations are highlighted by underlining and the start of each respective protein fragment indicated by an arrow.

1 atgccctggggggcctgctgcgcctctctcagtagccctggggggcggcgccctggggcagtcgcccgggggggcttggcggcggaggaaaggg  
17 M P V G G L L L P L F S S S T G G G G L G S G L G G G L G G R K G  
37 tcggcccgccctccgcctccgcctcaccggaagtgctctgctgctgctgcagccctccatccagctctgctctggccggcaccg  
33 S G P A A F R L T E K F V L L L C V F S A C F I T L C F G A I  
184 tcttctcctgctgacccctccagctgctcaggggggcctgctccctccacccttgccactgacggcccgggcagcacaaaggcggctc  
62 F F L P D S S K L L S G V L F H S N P A L Q P P A E H K P G L  
d65 primer  
278 ggagcgcctgcggaggtatgcgcggggggagtcggccggcggggggggcggcctgggggacccggggcggagctggaagacaacttagcca  
93 G A R A E D A A E A G R V R H R E E G A P G D P G A G L E O N L A  
d105 primer  
374 ggatccgcgaaaaccacgagcgggctctcagggagccaaaggagaccctgcagaagctcgccggaggagatccaaagacattcgcctggagagg  
125 R I R E N H E R A L R E A K E T L Q K L P E E I Q R D I L L E K  
470 aaaaaggcggccaggaccagctcgctgacgaagactcgctttaggggctcgcccaagtgaggacttccgcccccctggggtagagaaacggggggc  
157 E K V A O D O L R D K D L F R G L P K V G T D L P P V G V E N R E  
d187 primer  
566 ccgcgcgcgcacccatctcgcctgaggaaggggcgaagatcaagagagctgtagcccatgcttggggaataattataaacgcctatgctgctggggc  
183 P C A D A T I R E K R A K I K E M M Y H A W N Y I K R Y A W  
565 ttgaacgaacctgaacctatatcaaaaggagggccattcagccagtttcttggcaacatcaaggagctctacattagttagtg  
219 L N E L K P I S K E G H S S S L F G N I K G A T I V D  
737 cccctggatacccttttcattatgggcctgaagactgaatttcaagaagctaaatcgtggattcaaaaattatttagatkttaa  
246 A L D T L F I M G M K T E F Q E A K S W I K K Y L D F N  
815 tctgcaatcgctgaagtcttctcttttgaagctcaacatacctgctgctggagctgctctcagcctactatttcttcggagag  
273 V N A E V S V F E V N I R F V G G L L S A Y Y L S G E  
901 gagatatttccgaagaaagcagctgggaacttgggggtanaattgctacctgcttccactcctccttggaaatccttgggcct  
301 E I F R K K A V E L G V K L L P A F H T P S G I P W A  
983 tgcctgaatgaanaagctgggactcggggcgaacttgggcttgggagcagcagctatcccttggccgaattctgggaactct  
328 L L L D K K S G I G R N W P W A S G G S S I L A C Y G T L  
1065 gcattttagmkttatgctcatttccacccttatcaggagaccagctcttctggccanaagggttatgaanaattcggaatagctgt  
335 H L E F M H L S H L S G D P V F A E K V M K I R T V L  
1147 nacaaactgkcaaacacaggaagcctttatctcactatctgaacccagctagtggagactggggctcaacatctatgctgctgg  
383 N K L D K P E G L Y P N Y L N P S S G Q W G Q H V S  
1229 ctggaggacttgggaacacgcctctcatgaattattgttaaggcgtggttaagtgtatgaanaagacagatctcgaagcaagaa  
410 V G G L L G D S F Y E Y L L K A L M S D K T D L E A K K  
1311 gatgtatttctgctgctgttcaggccctcagagactcatttgcctccgcaagtcagggggactaactgtacatcgcgcagctgg  
437 M Y F D A V Q A I E T H L I R K S S G G L T Y I A E W  
1392 aaggggggcccctctggaatacaagatggggccactctgctgcttctcaggaggcagctgttgcacttggggcagatggagctc  
465 K G G L L E H K M G H L T C F A G G M F A L G A D G A  
1475 gggaagccggggcccaactcactctgaactcggagctgaanaattgcgcgcgacttctcagtgactcttatatctgtacatctgt  
493 P E A R A Q H Y L E L G A E I A R T C H E S Y N R T Y V  
1557 gaagtgtggaccggaagcgttttcgatttgctggcgtgtggaagctatgtccacggagccaaatgaanaagatttaccatctta  
519 K L G P A C F R F D G G G V E A I A T R Q N E K Y I L  
1639 cggcccgaggtctatcgagacatcatctgtacatgtggcgactgactcaagaccccaagtagcaggatcttgggcttgggaagccg  
547 R P E V I E T Y M M W R L T H D P K Y R T W A W E A  
1721 tggaggtctctagaaggtcactgcagagtgaacggaggtcactaagctcactcaggtatgtttacattccggctgagagtattga  
574 V E A L E S H C R V N G G Y S G L R D V Y I A R E S Y D  
1803 cgatgtccagcaagctttcttctggcagagacactgaagtatttgctactgttactatttccgatgtatgaacttcttccacta  
601 D V Q Q S F F L A E T L K Y L Y L I F S D D D L L P L  
1885 gaacactgtgattctcaacacccaggctcattcttccctatctcctgcgcagcaaggaaggaaattgagggcaagagaaatga  
629 E H W I F N T E A H P F I L R E Q K K E I D G K E A

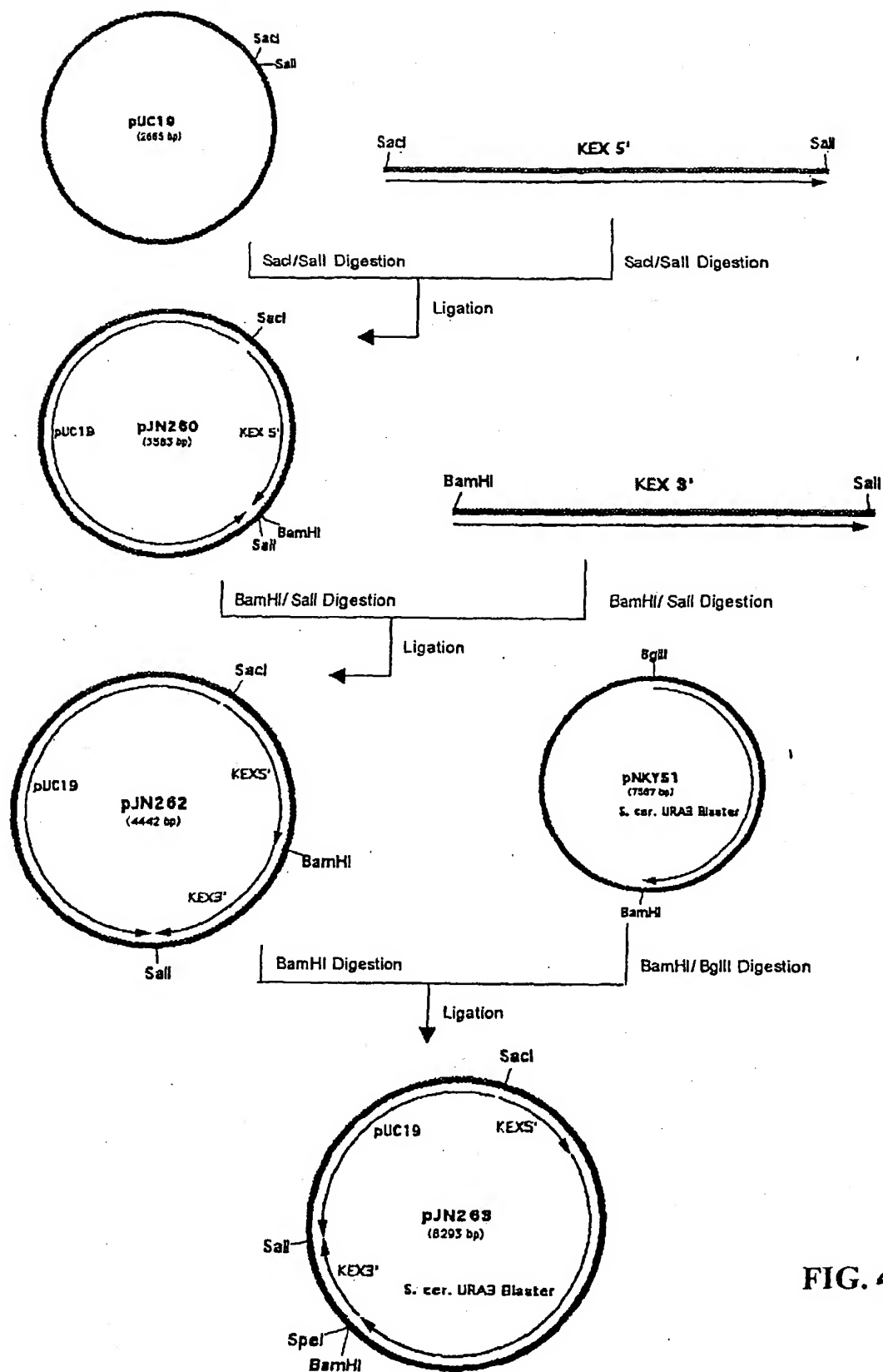
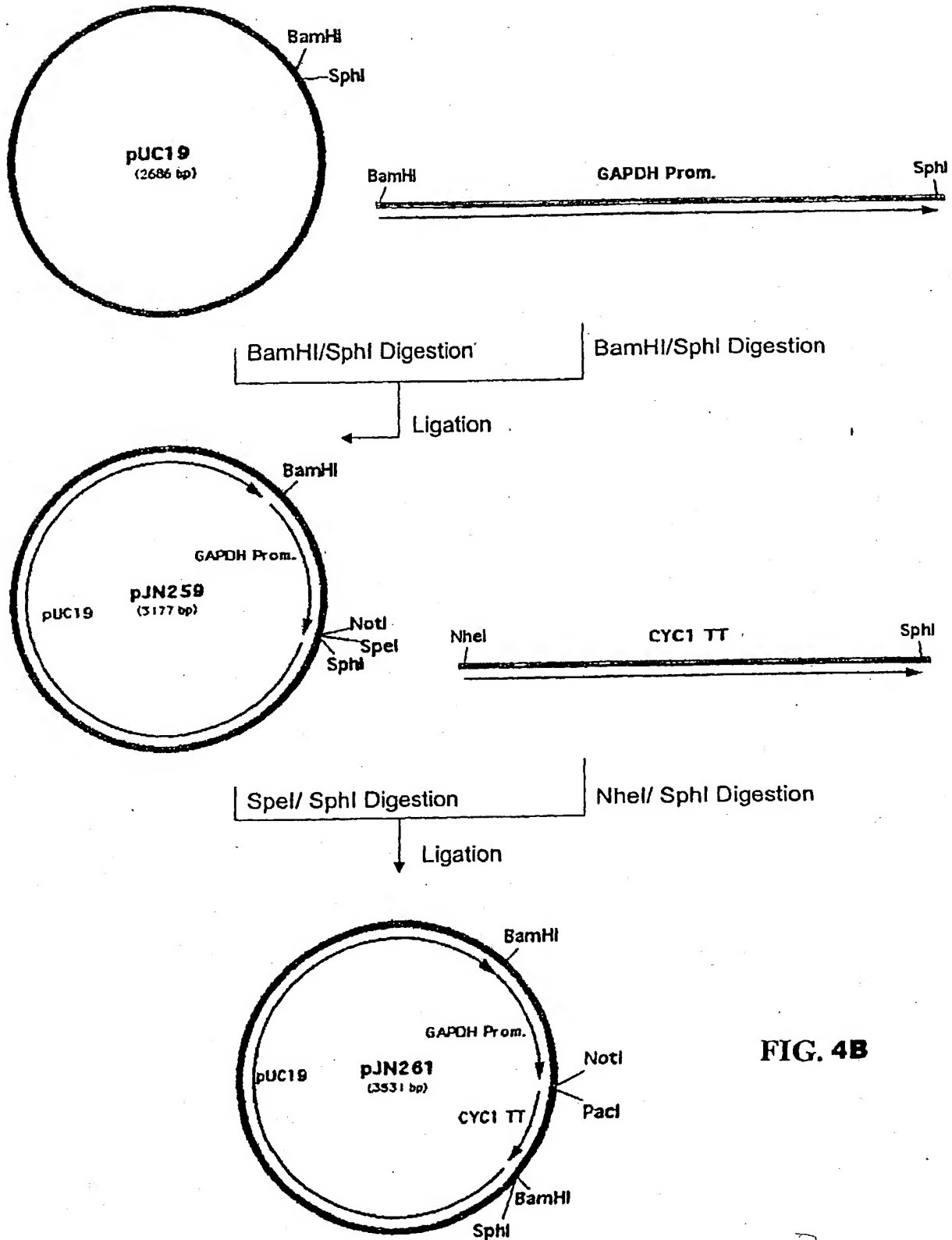


FIG. 4A



**FIG. 4B**

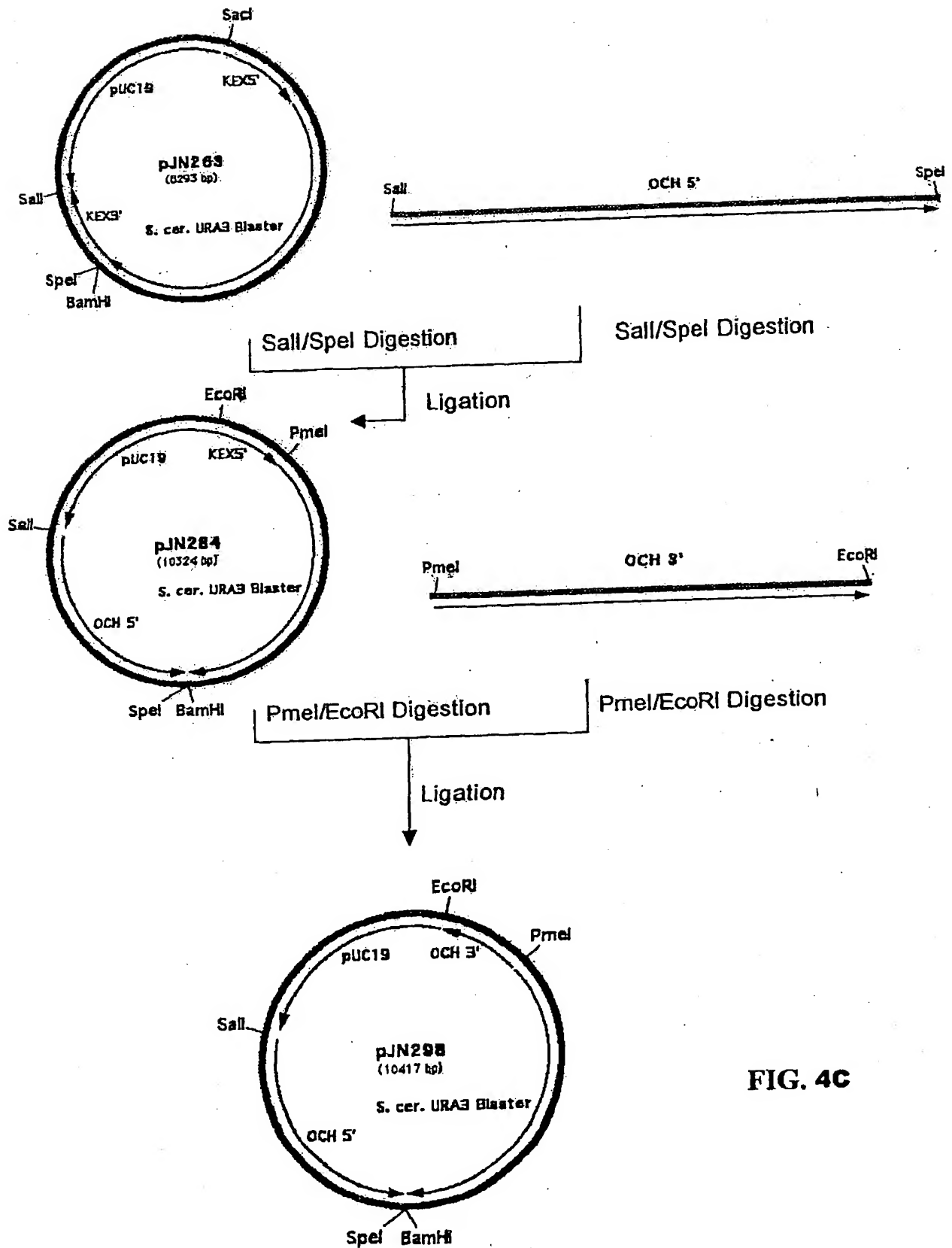
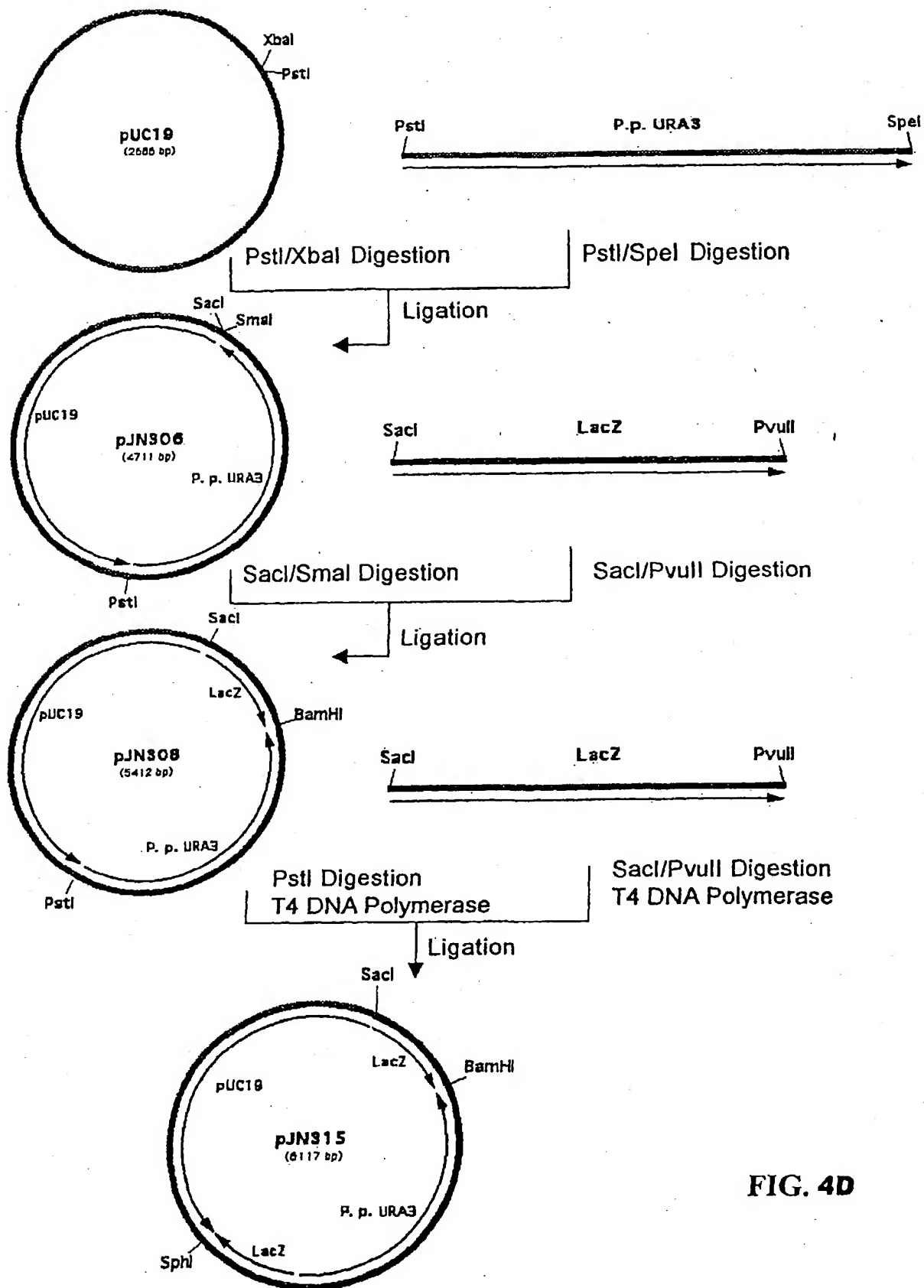


FIG. 4C



**FIG. 4D**

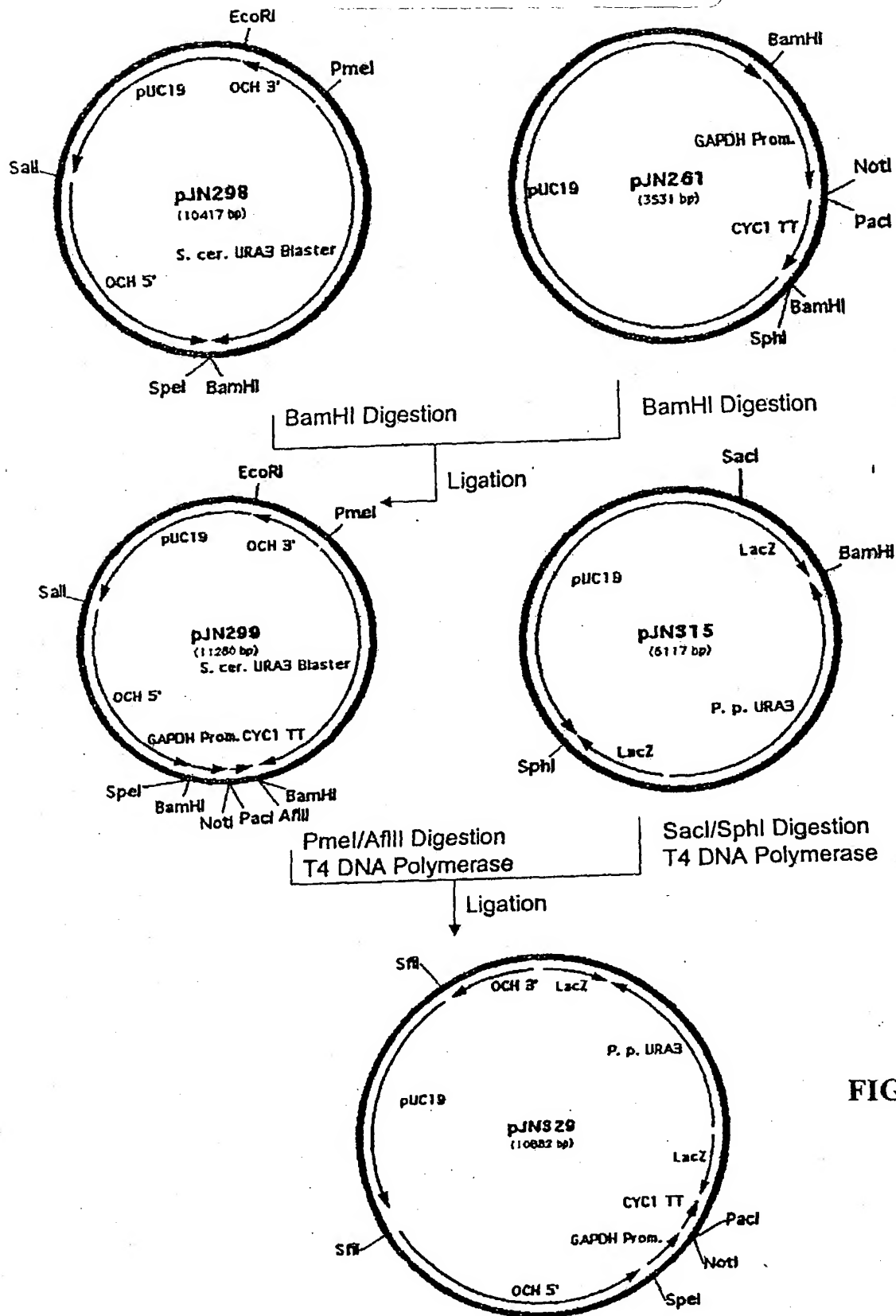


FIG. 4E

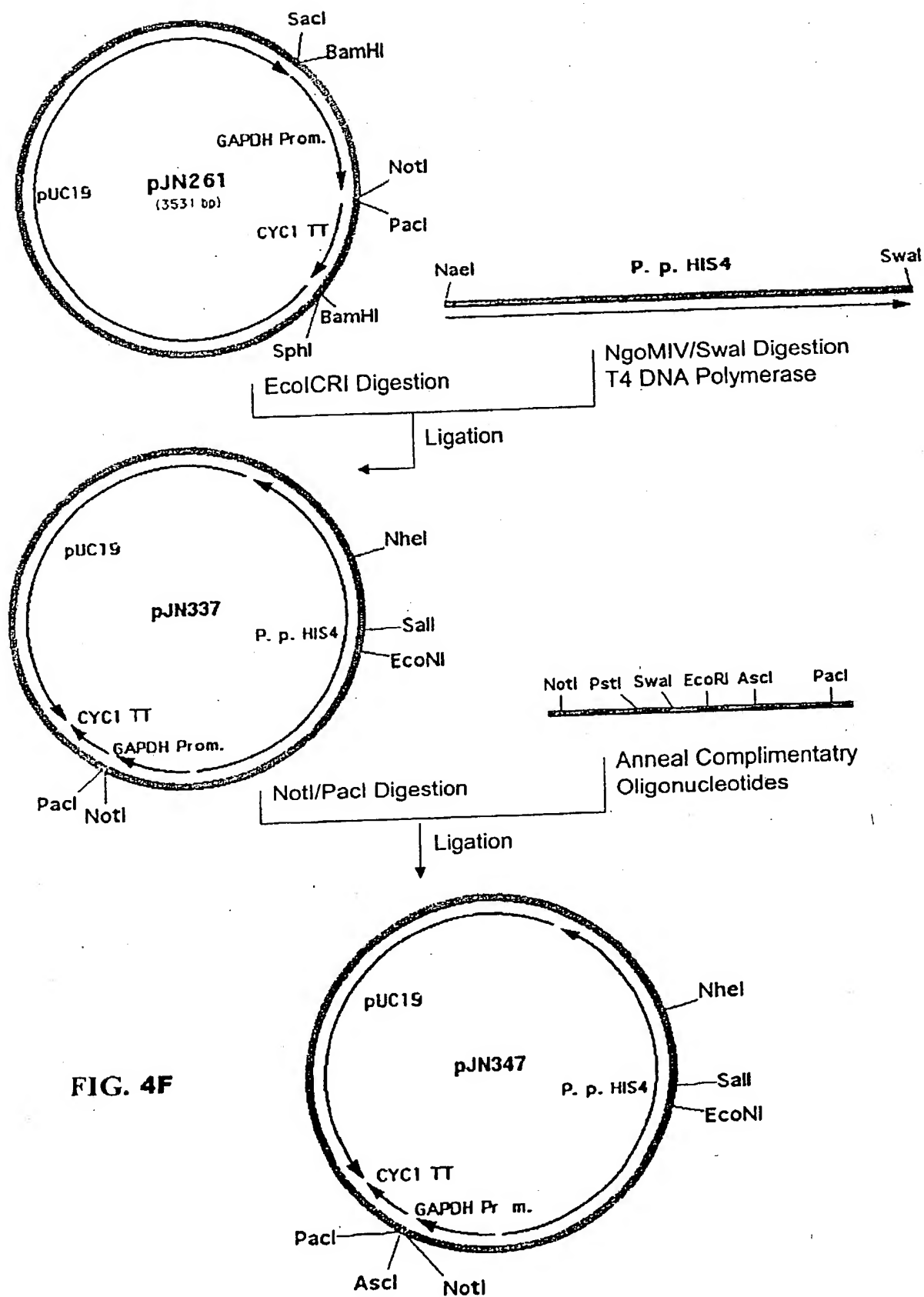


FIG. 4F

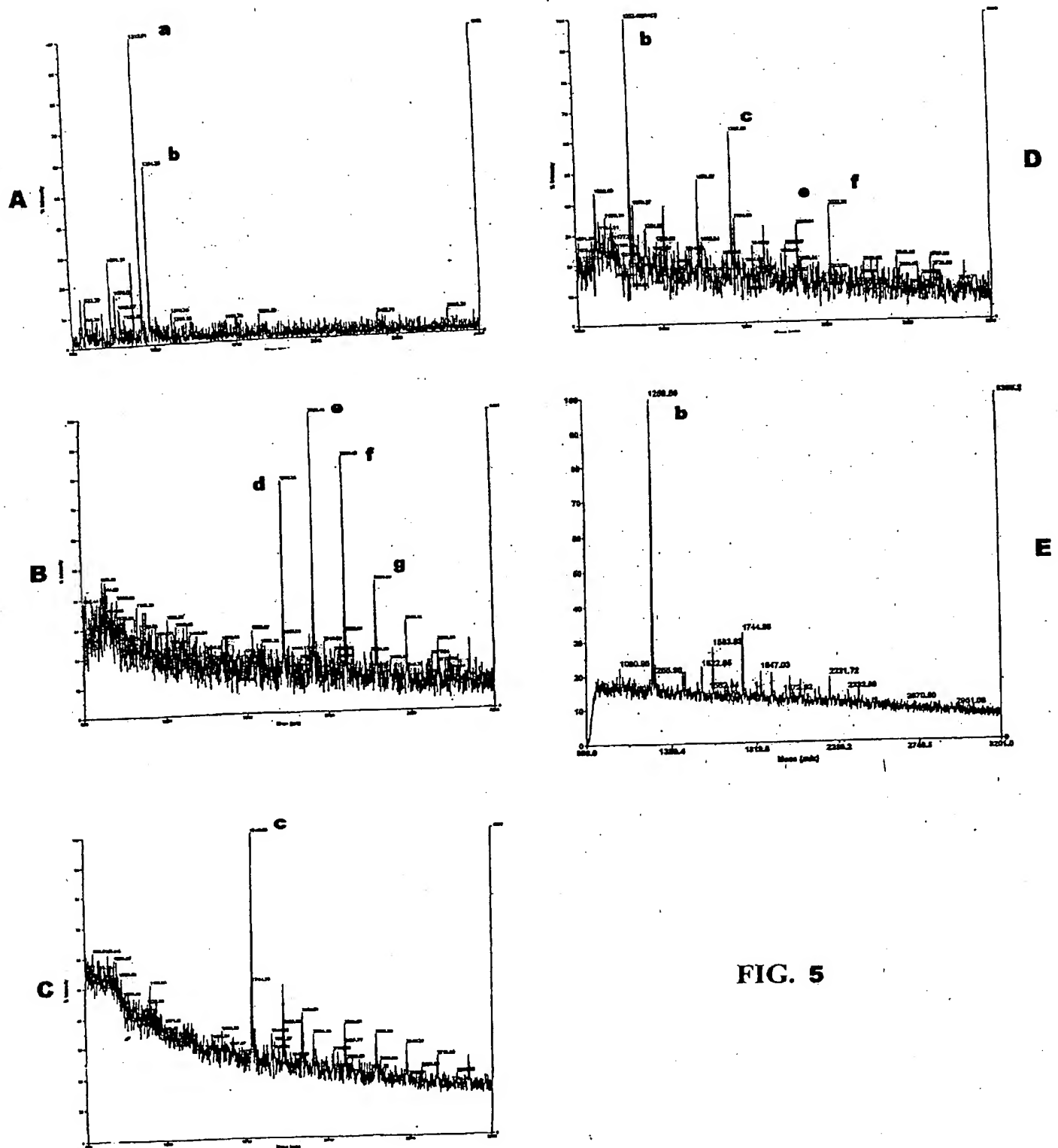
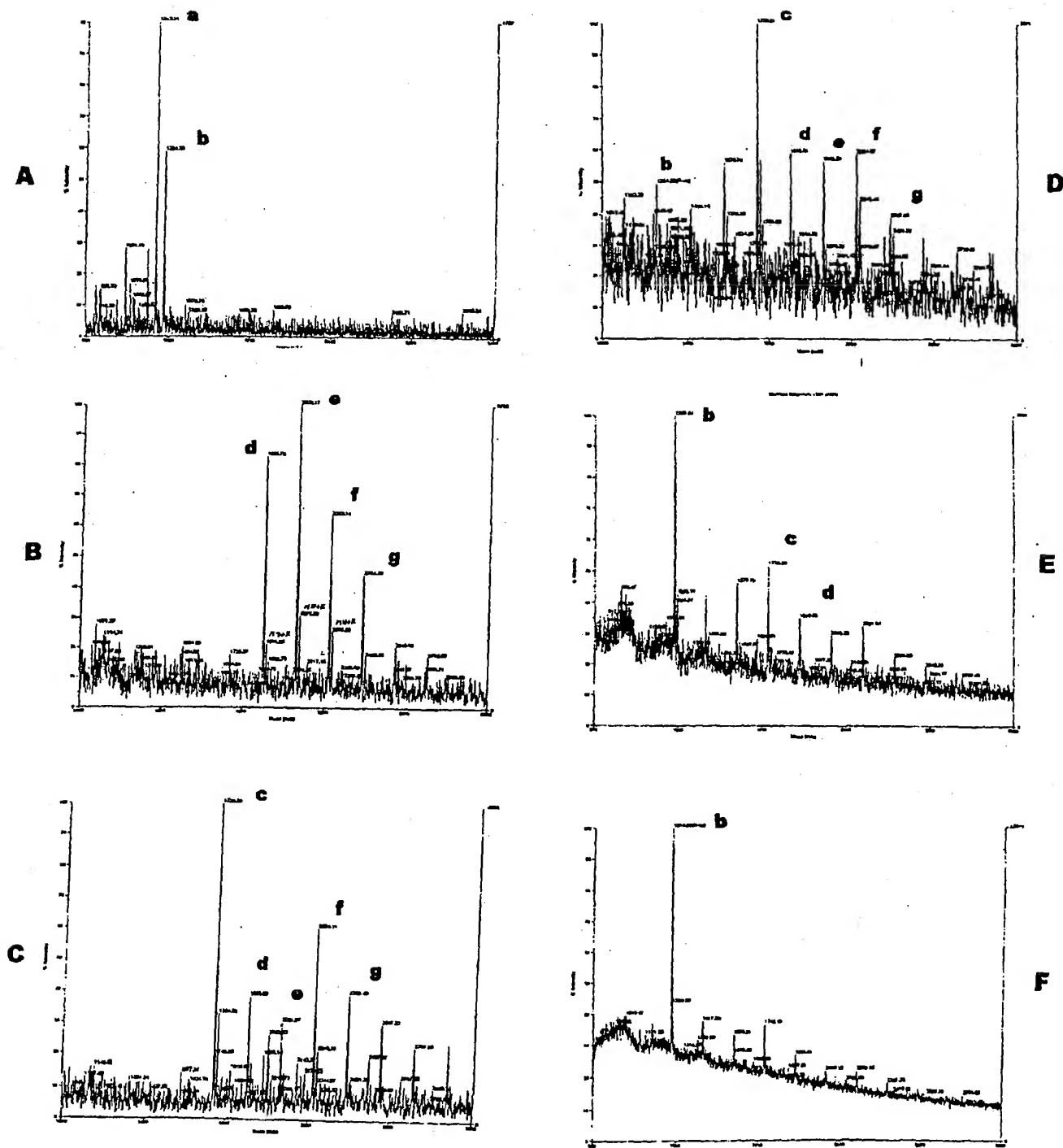
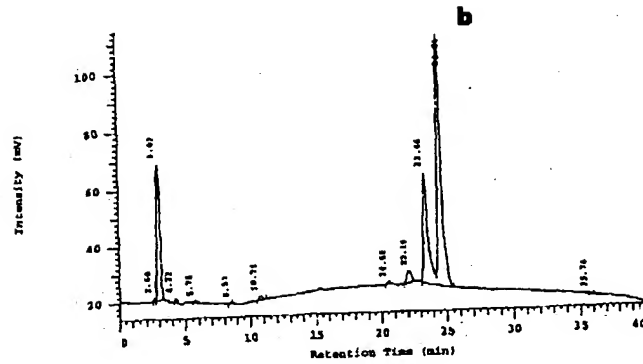


FIG. 5

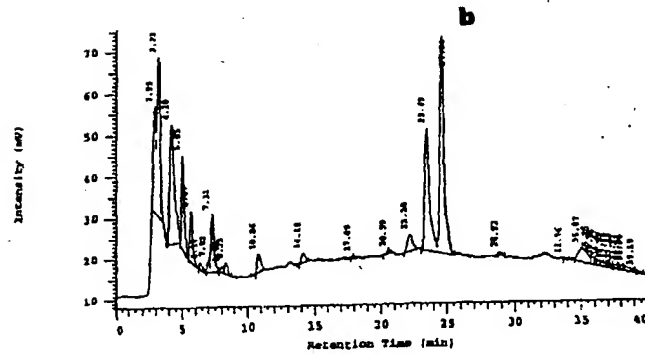
FIG. 6



A



B



C

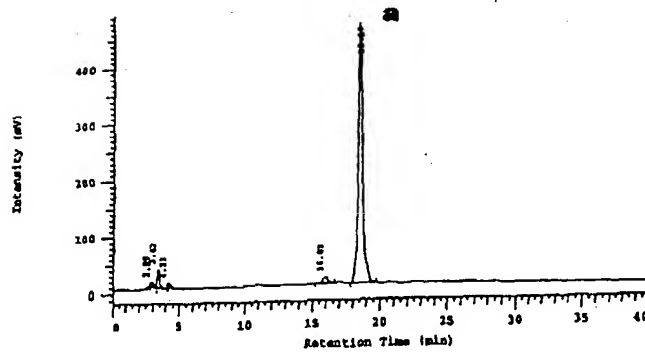
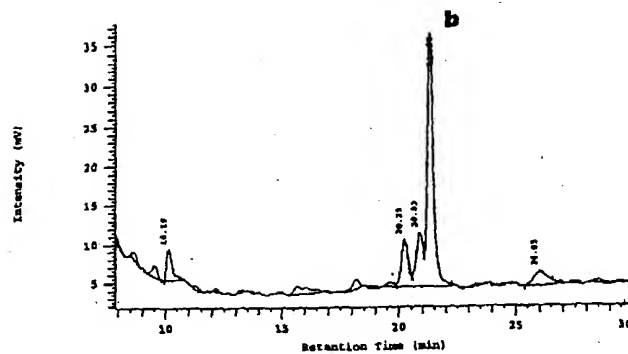
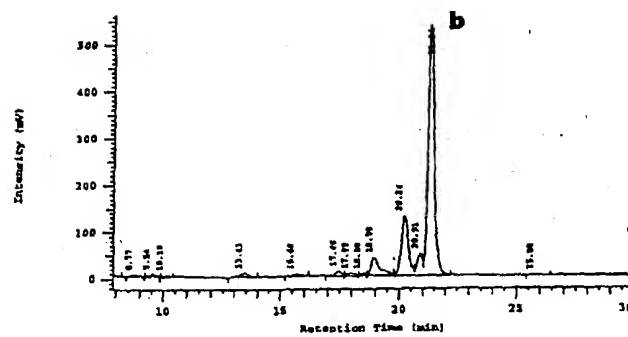


FIG. 7

A



B



C

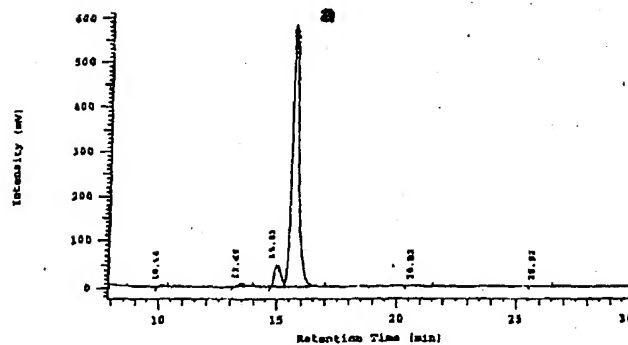
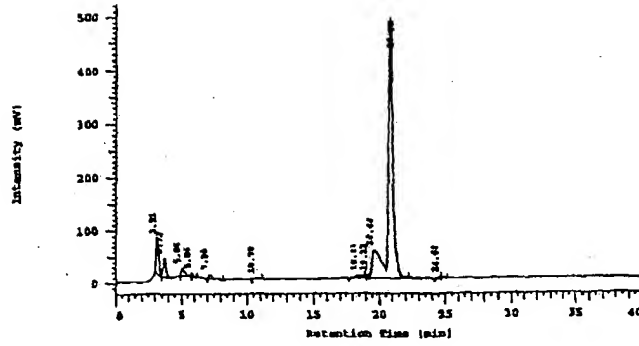
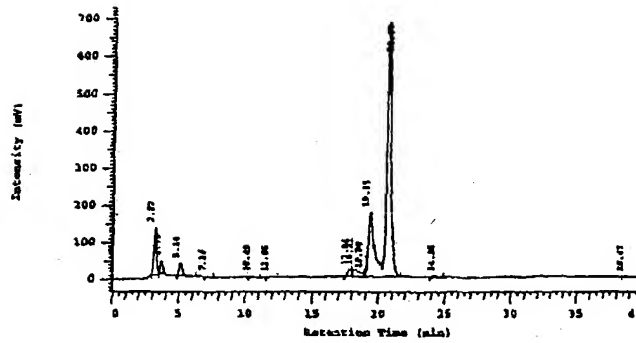


FIG. 8

A



B



C

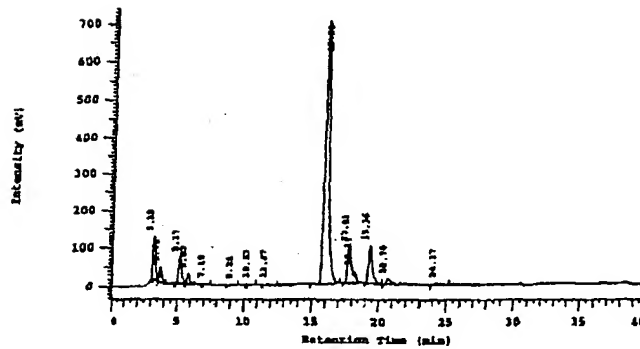
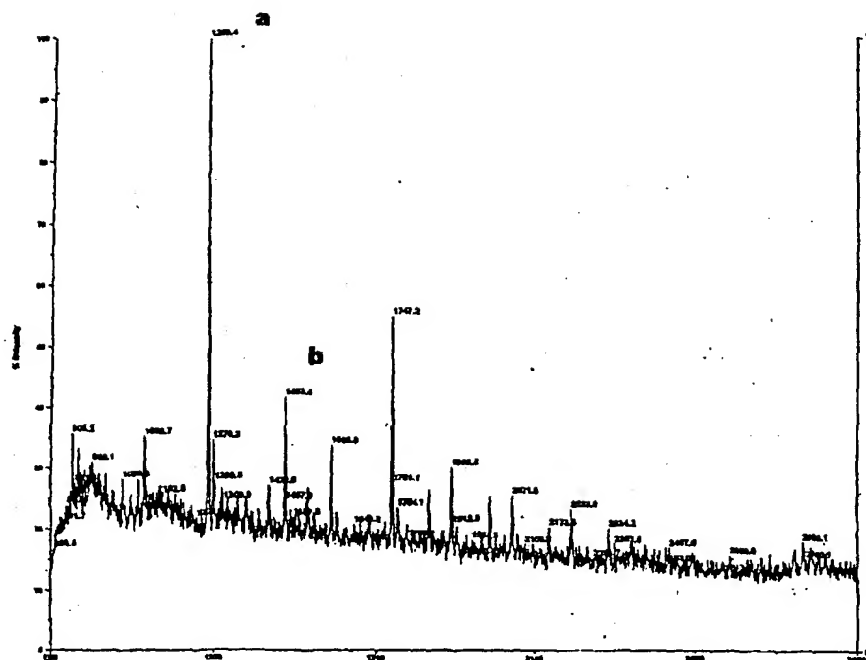
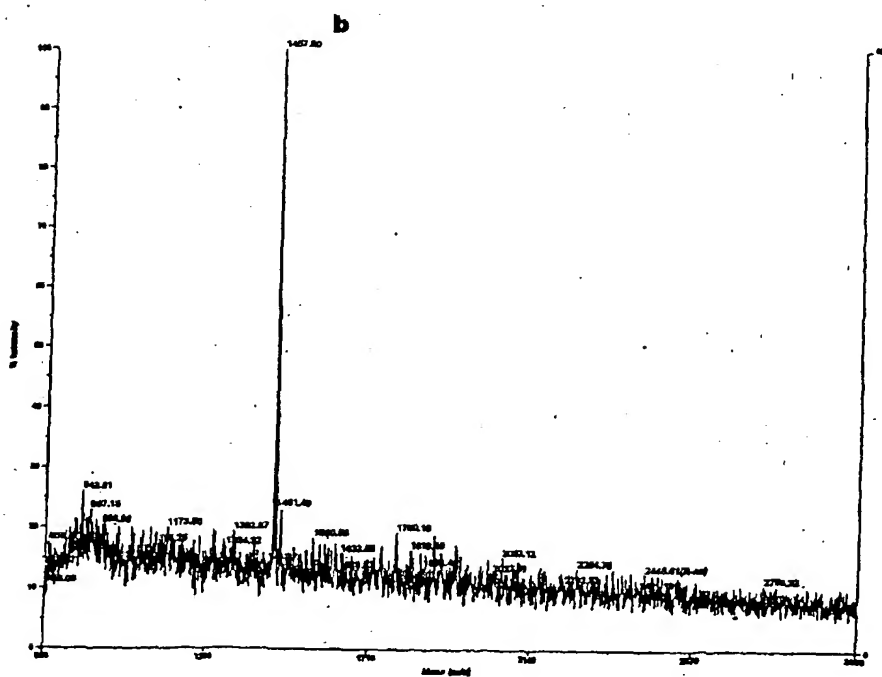


FIG. 9

**FIG. 10**



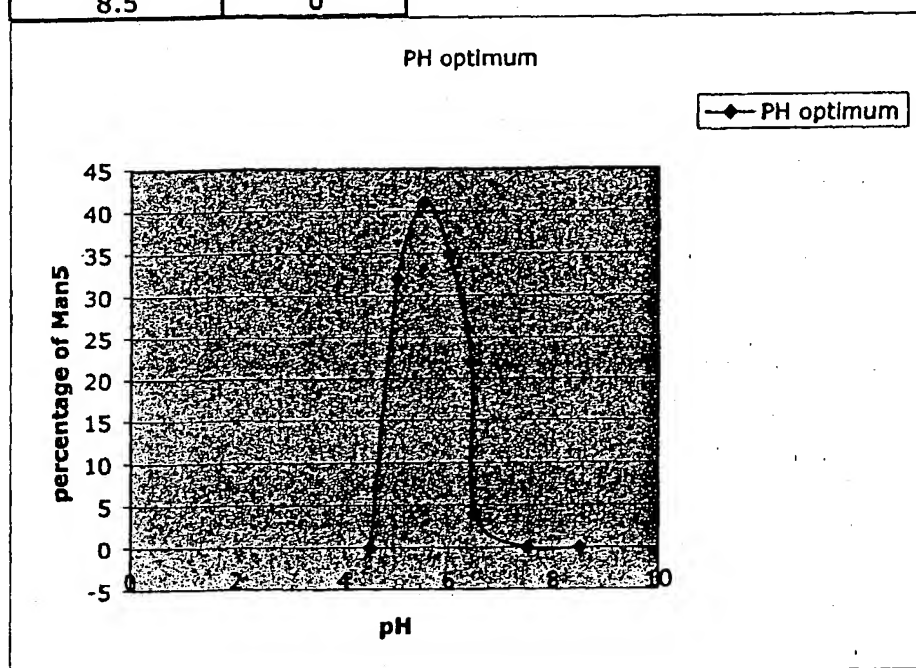
**A**



**B**

**pH optimum for BB27-2 medium**  
**C. elegans Mann1B D31 and S. Mnn10-s**

pH	% of Man5
4.5	0
5	32
5.5	41
6	35
6.43	22
6.5	4
7.5	0
8.5	0



**FIG. 11**

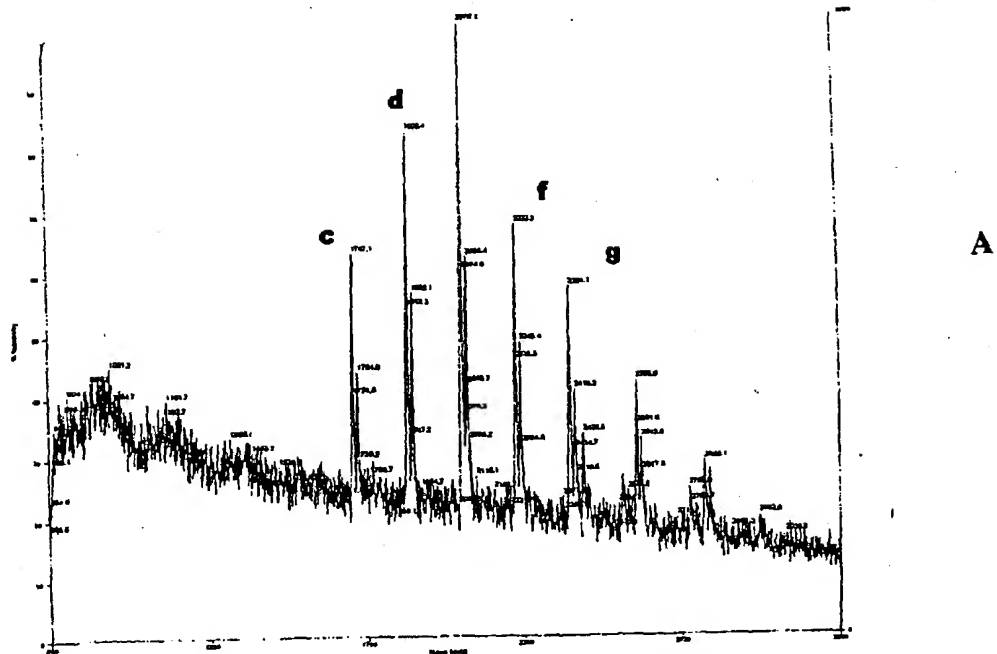
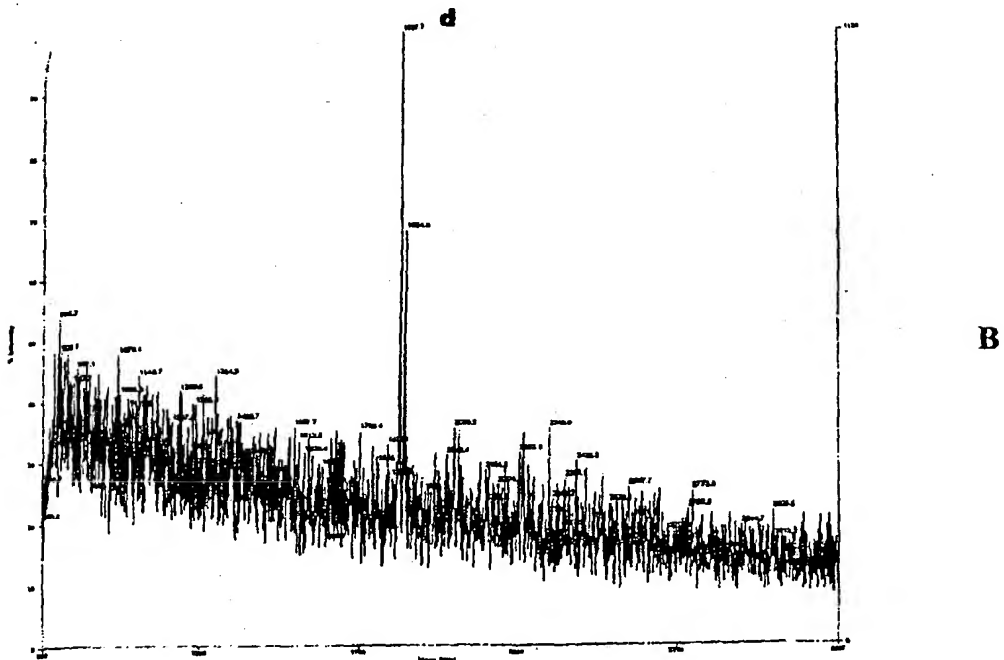


FIG. 12



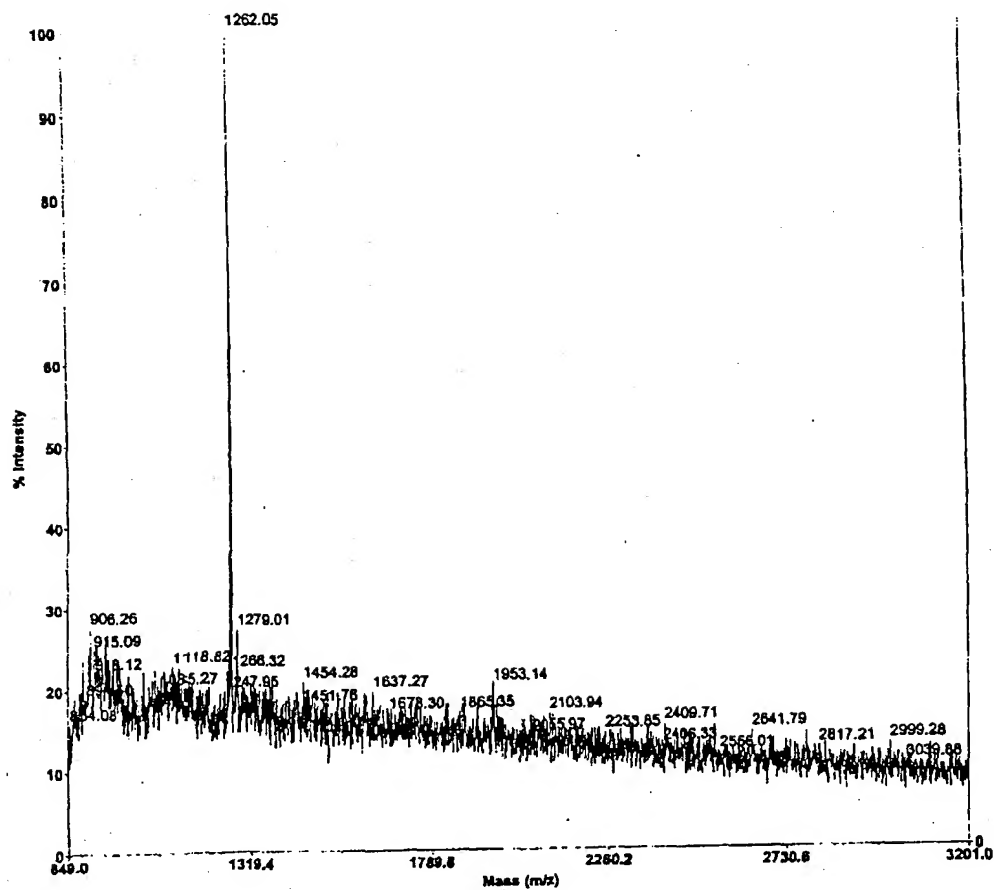


FIG. 12C

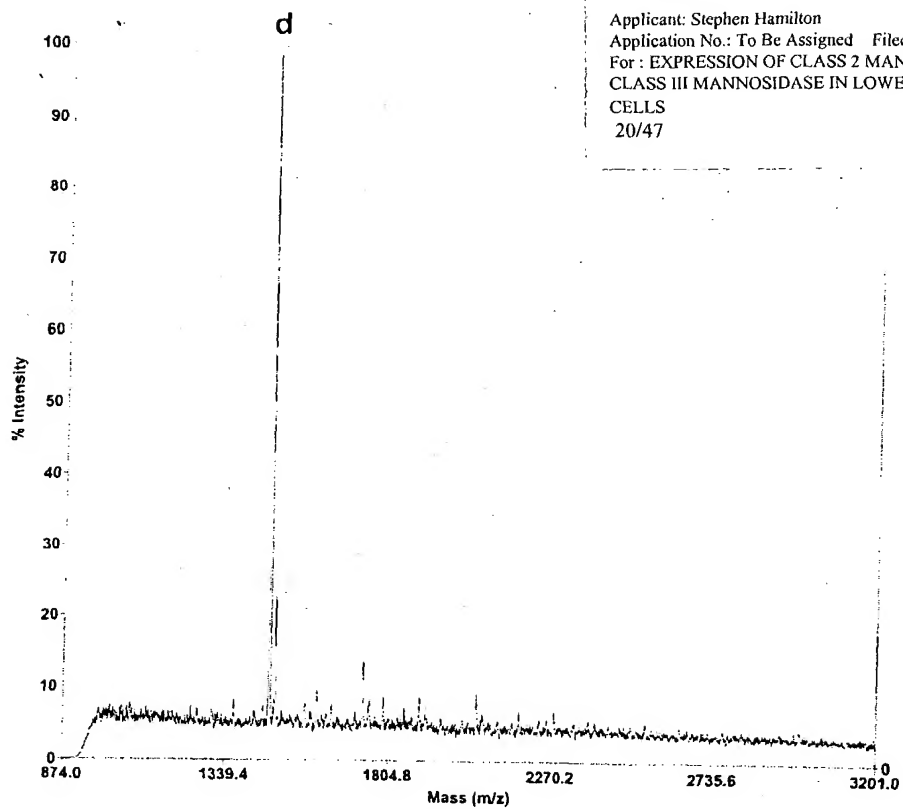


FIG. 13

Applicant: Stephen Hamilton GFI-107  
Application No.: To Be Assigned Filed: Herewith  
For: EXPRESSION OF CLASS 2 MANNOSIDASE AND  
CLASS III MANNOSIDASE IN LOWER EUKARYOTIC  
CELLS  
21/47

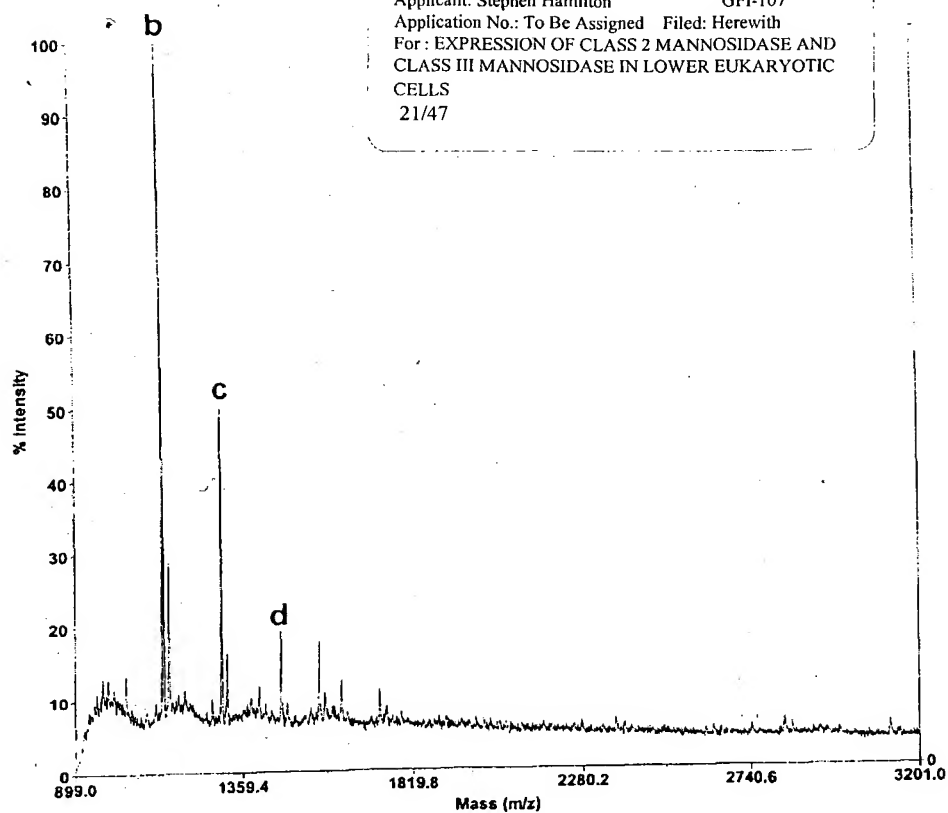
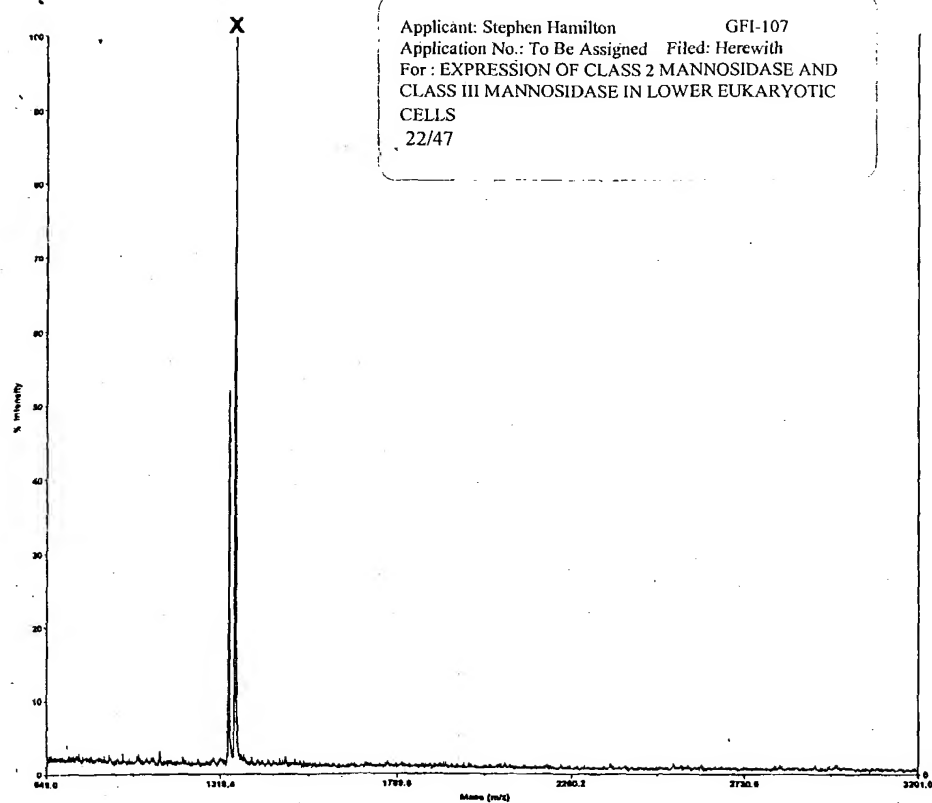
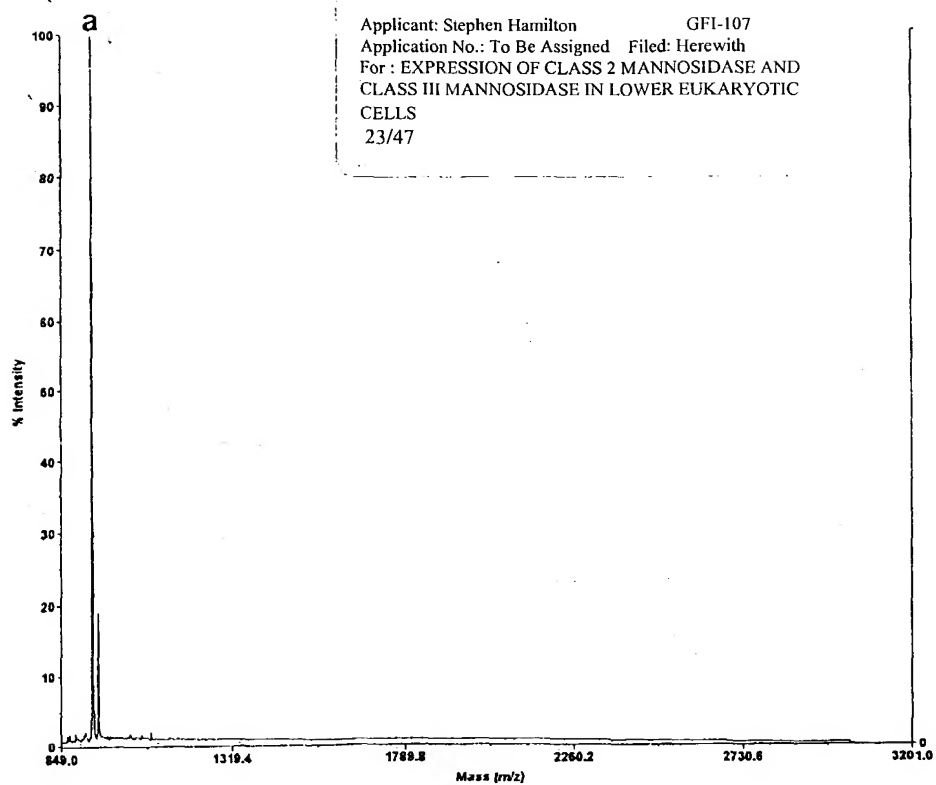


FIG. 14



**FIG. 15**



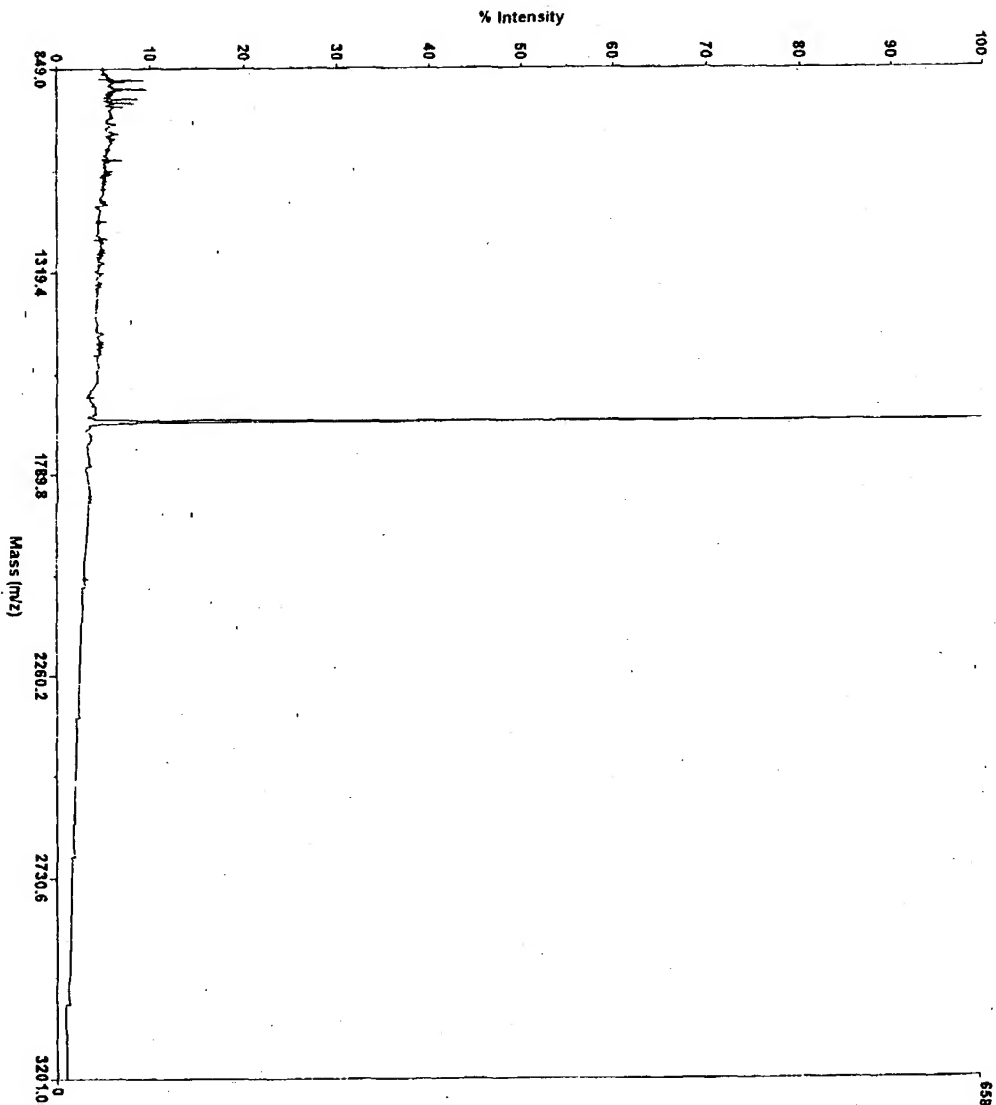
**FIG. 16**

Applicant: Stephen Hamilton  
 Application No.: To Be Assigned Filed: Herewith  
 For: EXPRESSION OF CLASS 2 MANNOSIDASE AND  
 CLASS III MANNOSIDASE IN LOWER EUKARYOTIC  
 CELLS  
 24/47

FIG. 17

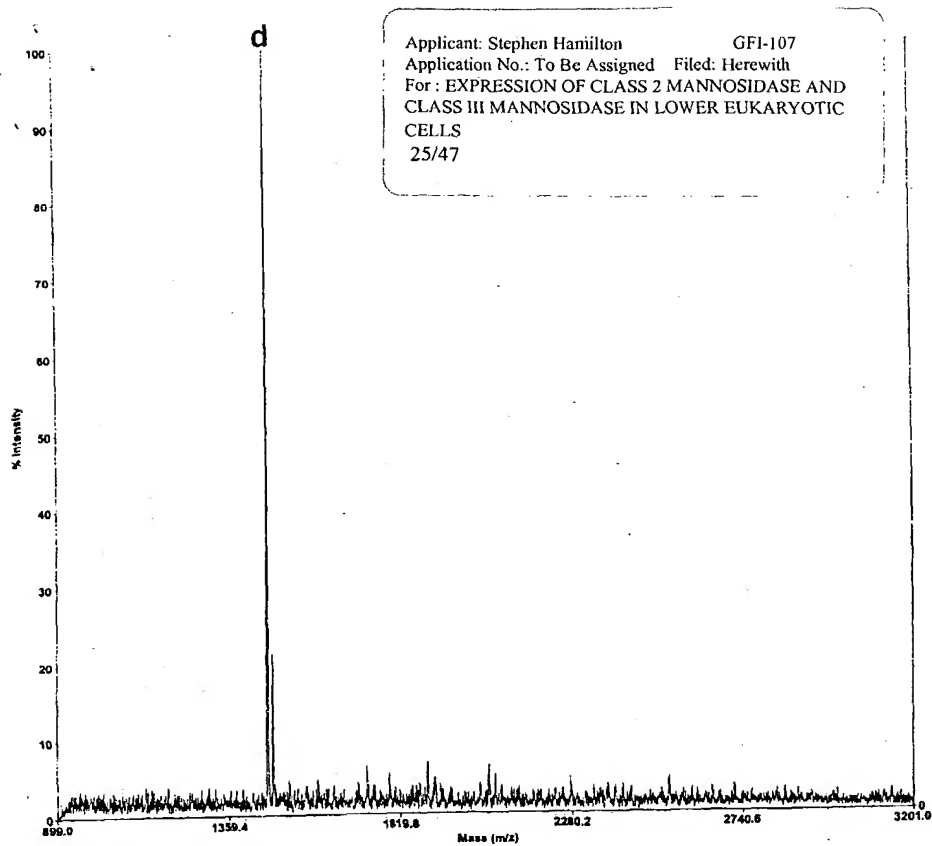
Applied Biosystems Voyager System 1246

Voyager Spec #1=>BC=>NR(2.00)[BP = 1664.6, 658]

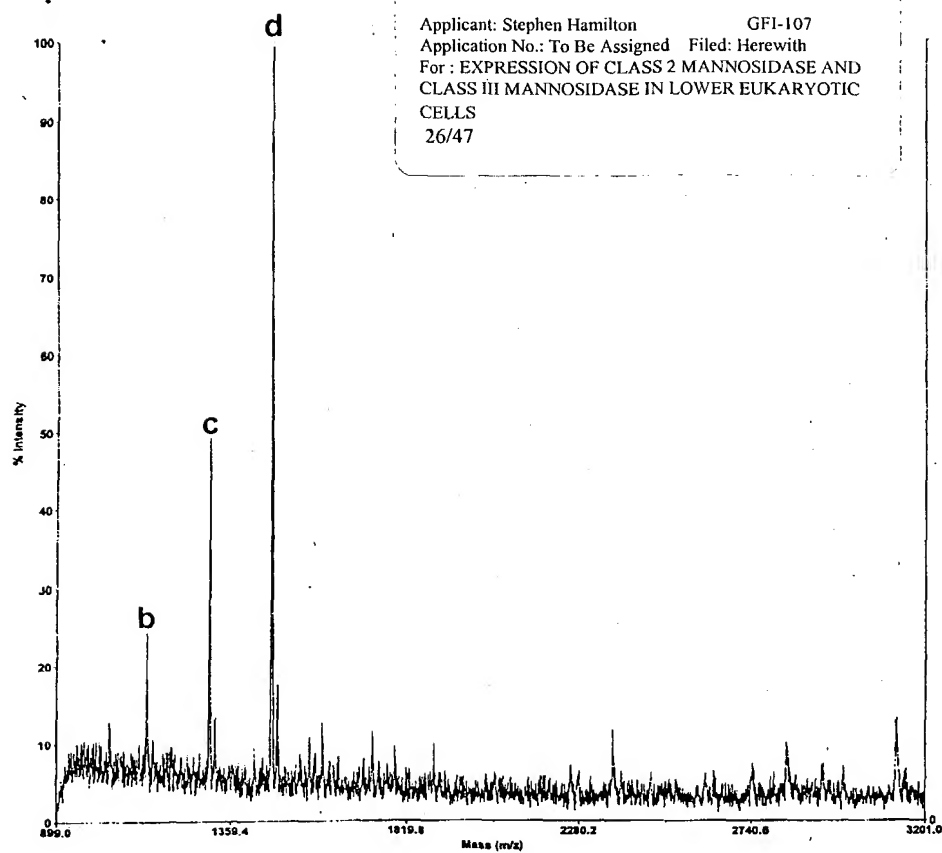


Acquired: 10:12:00, June 13, 2003  
 D:\GLVCO-F1\DATA\Yujuan Data\Other samples\June 2003\HL\_6-13-03 Gal Transfer\6-2-03 SH MIV GN2M3 + GalT Sol\_0001.dai

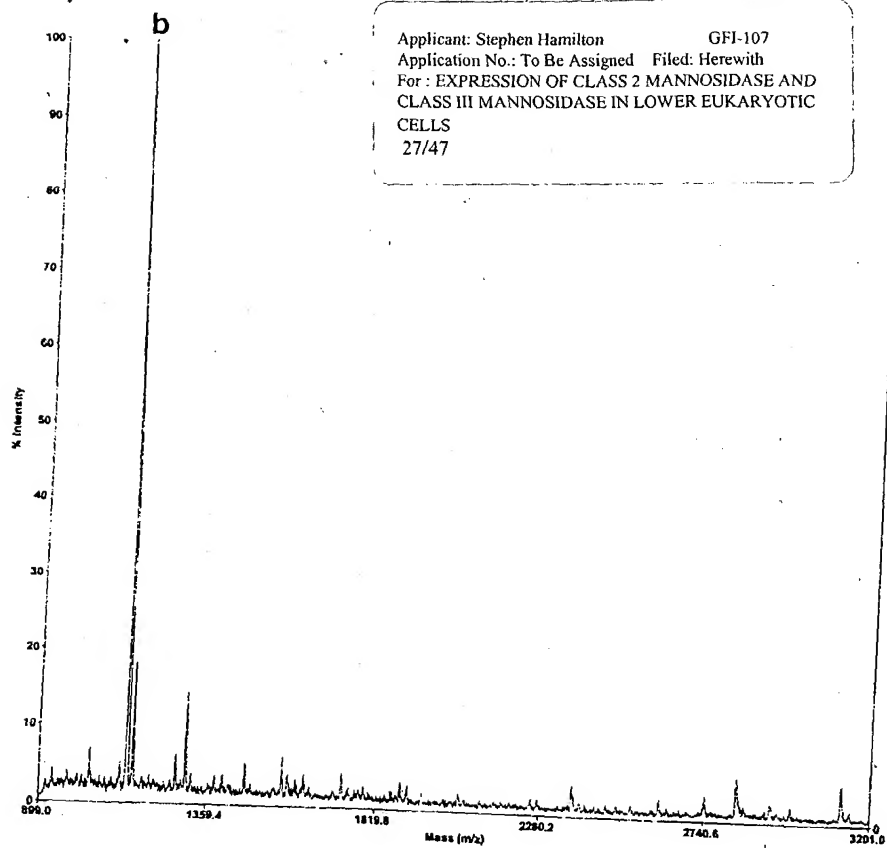
Mode of operation: Linear  
 Extraction mode: Delayed  
 Polarity: Positive  
 Acquisition control: Manual  
 Accelerating voltage: 20000 V  
 Grid voltage: 94%  
 Guide wire D: 0.05%  
 Extraction delay time: 100 msec  
 Acquisition mass range: 850 - 3200 Da  
 Number of laser shots: 100/spectrum  
 Laser intensity: 2713  
 Laser Rep Rate: 20.0 Hz  
 Calibration type: Default  
 Calibration matrix: 2,5-Dihydroxybenzoic acid  
 Low mass gate: 800 Da  
 Digitizer start time: 18.582  
 Bin size: 2 msec  
 Number of data points: 8676  
 Vertical scale: 500 mV  
 Vertical offset: 0%  
 Input bandwidth: 150 MHz  
 Sample well: 47  
 Plate ID: 100 WELL PLATE  
 Serial number: 1246  
 Instrument name: Voyager-DE  
 Plate type filename: C:\VOYAGER\100 well plate.p  
 Lab name: PE Biosystems  
 Absolute x-position: 31305.6  
 Absolute y-position: 28089.3  
 Relative x-position: -761.973  
 Relative y-position: 1081.83  
 Shots in spectrum: 100  
 Source pressure: 4.393e-007  
 Mirror pressure: 0  
 TC2 pressure: 0.004253  
 TIS gate width: 30  
 TIS flight length: 940



**FIG. 18**



**FIG. 19**



**FIG. 20**

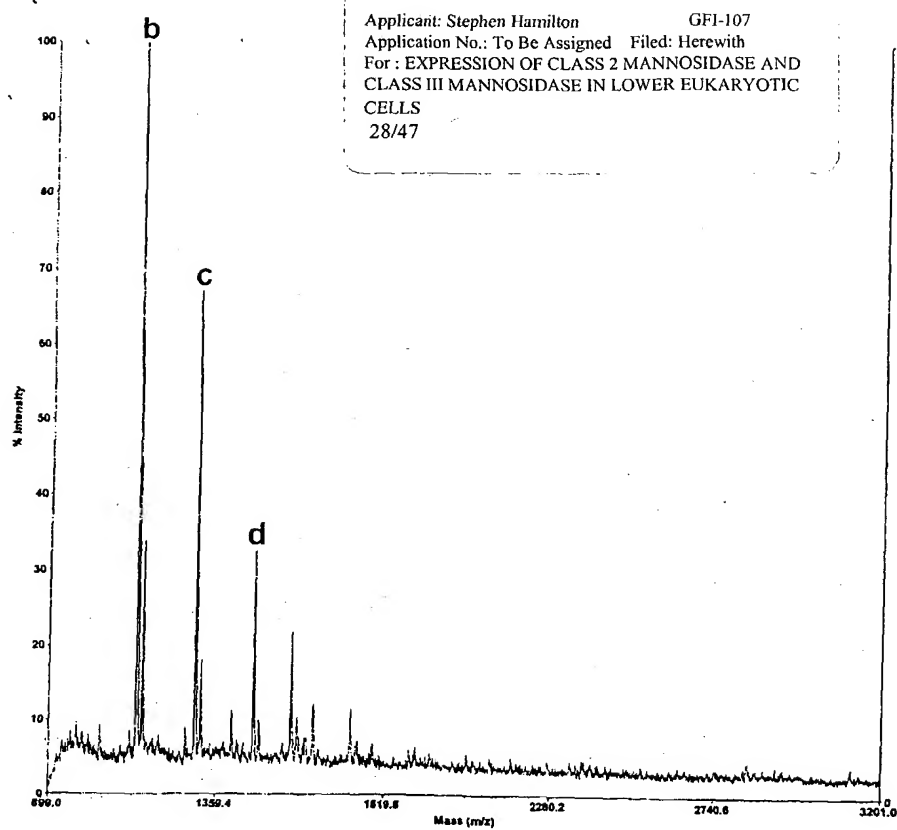
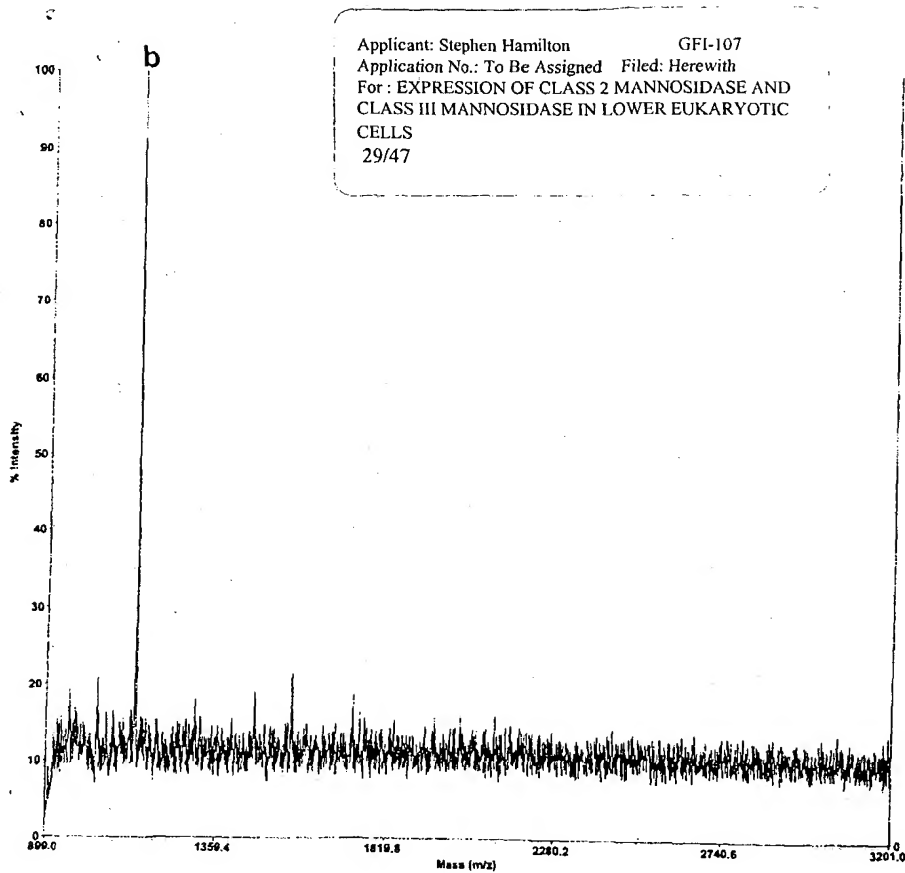


FIG. 21



**FIG. 22**

# Biology WorkBench

click here to  
toggle between  
menus and buttons

WE  
Moved! <http://workbench.sdsc.edu/>

Version 3.2

## BOXSHADE

Color-Coded Plots of Pre-Aligned Sequences

### Selected Sequence(s)

- Drosu MannII (X77652),  
C.elegans MannII,  
rMannII (XM\_218816.1),  
hMannIIx D55649,  
Mouse MannII (X61172),  
human MannII (U31520),  
CionaMannII (AK116684),  
ArabMannII,  
Insect ManIII,  
hLyso MannII,  
hCyto MannII (NM\_006715)

[Return](#) [Help](#) [Report Bugs](#)

Download a PostScript version of the output

```
Droso_MannII_[X] 1 -----
C.elegans_MannI 1 -----
rMannII_[XM_218] 1 MACIGGAGGQGRQAVREKIPSHQGYPMRMTNGSCSEHALLSKTRMYCHQGCVRPPETDVKN
hMannIIa_D55649 1 -----
Mouse_MannII_[X] 1 -----
hMannII 1 -----
CionaMannII_[AR] 1 -----
ArabMannII 1 -----
Insect_MannIII 1 -----
hLyso_MannII 1 -----
hCyto_MannII_[N] 1 -----

Droso_MannII_[X] 1 -----MSTTRRFAALVICSGCLVFLSLTILNFAAP-----AATQIRP
C.elegans_MannI 1 -----MGRLEYILCLG-VFLTVSLIYNGIETG-----ARALTKR
rMannII_[XM_218] 61 PFTTTDTQSVPGVSTLRVNTCCGAATPCATPSLIMIDRVQHDPAR-HQNGCNPPRS
hMannIIa_D55649 1 -----VLRVNTCCGAATPCATPSLIMIDRVQHDPT-RHQNGCNPPRS
Mouse_MannII_[X] 1 -----VLSVNTVFGSAIFCVSLIIMIDRGHLDYPRGPRRQSGFPQG
hMannII 1 -----VLSVNTVFGSAIFCVSLIIMIDRGHLDYPRNPRRQSGFPQG
CionaMannII_[AR] 1 -----VLSVNTLFGGIIITFGSLTIFIGOLD--TPNSPQIVAFSEGSIND
ArabMannII 1 -----MPFSSTYCHSRSSSTGGGTGCGNGQSILP-----TALSRSKL
Insect_MannIII 1 -----MRTVLRCEPSTRILNITPLAVG-----V
hLyso_MannII 1 -----
hCyto_MannII_[N] 1 -----MAAPFLKHRTTPERELVSEYFTDCNLR-----G

Droso_MannII_[X] 40 EYENEMRELENGHCHEGHEMRNREARAKTNRD-----
C.elegans_MannI 37 CANDURREGNLERVAENGRTIDRLEONORAKAKSVDFDKEHKTRREHVEKKKRV
rMannII_[XM_218] 120 QSVLONTECLECLBENREIISHKDSLELANAGPPALLPY-----
hMannIIa_D55649 46 QSVLONTECLECLBENREIISHKDSLELANAGPPAMLPY-----
Mouse_MannII_[X] 47 QSVLONTECLECLBENREIISHKDSINLSVEDGPRGSPG-----
hMannII 47 QSVLONTECLECLBENREIISHKDSINLSVEDGPRSSQS-----
CionaMannII_[AR] 45 QVTLQDRSLTFRRLIENRMRKSDODPMNKHVPMQGHIR-----
ArabMannII 37 AMNRKPRRTLVVVFPAVFFIALTVSLTFLTFPFGVPGPIG-----
Insect_MannIII 28 YCIFYNAPQNYNPRISTYPAGNEHFRSSSTRTV-----
hLyso_MannII 1 -----NGYAAASGVCAR-----
hCyto_MannII_[N] 34 RYFGASCPNAVSSSPITPERLPYQRAVQDPRPAQVG-----

Droso_MannII_[X] 77 -----DPIRPPLEVARSPRPGCCQVVQDVPHVQCMERATERNSTRDIN
C.elegans_MannI 97 APVPVVRGNGEMARHQVQRIRPTPSMDVCGIRENVSIARSDQMDATMTWRFNPI
rMannII_[XM_218] 166 HTANGSAVLPEPRPEPPVSPEDQFALGGRGQRPDMITASIRPPDHV
hMannIIa_D55649 92 YTVGSMVVPPEPRPFAFFGISPDQFALGGRGQRPDMITASIRPPDHV
Mouse_MannII_[X] 93 FASQGS-IHLSPQLA-LQADPRDLFASQSGSQPRQMDATMTWRFNPI
hMannII 93 FASQAGSHLLPSQLA-LEVDTADLFASQSGSHNSQMDATMTWRFNPI
CionaMannII_[AR] 94 NVVREPVLPFLINGQFANDSRMSDTCPLVSYSGGASQVKNMATERPPDPE
ArabMannII 83 -----SRFLTSRSHRIVEPRMIRPRINDSNAGAVVTTEDATRELDTH
Insect_MannIII 63 -----SRDEPTDQCPALRESEADIDTA YPTLPQPSMIR
hLyso_MannII 13 -----GCILSAGPWMTSERALRPPLP CPFLLLAAGAR
hCyto_MannII_[N] 71 -----DSFGPTWTCFPRVELTIPAN GQEVHLCMSDGC

Droso_MannII_[X] 122 SGVMROGMLTLPKFNABRE-LVFFVVPESHMTPE-----QV
C.elegans_MannI 157 SGVMROGMLTLPKFNABRE-LVFFVVPESHMTPE-----MT
rMannII_[XM_218] 219 SGVMROGMLTLPKFNABRE-LVFFVVPESHMTPE-----RT
hMannIIa_D55649 145 SGVMROGMLTLPKFNABRE-LVFFVVPESHMTPE-----RT
Mouse_MannII_[X] 144 SGVMROGMLTLPKFNABRE-LVFFVVPESHMTPE-----RT
hMannII 145 SGVMROGMLTLPKFNABRE-LVFFVVPESHMTPE-----RT
CionaMannII_[AR] 147 SGVMROGMLTLPKFNABRE-LVFFVVPESHMTPE-----RT
ArabMannII 132 SGVMROGMLTLPKFNABRE-LVFFVVPESHMTPE-----RT
Insect_MannIII 101 KEFQASDQRYRIHTTTPRDLVFFVVPESHMTPE-----RT
hLyso_MannII 48 EGTETCPTEPH-----MAYLATEHEDV-----RT
hCyto_MannII_[N] 107 SIVNDKPPQGLTKGRTS--YLTDRLGMDPS-----LTLY

Droso_MannII_[X] 162 FERTQ-----HDKRITSHARRHFERMFIWAESFALRDGERLIC
C.elegans_MannI 197 FERTQ-----RCRRLDGMARRHADEMFIWAESFETRDOADEIKV
rMannII_[XM_218] 277 FERTQ-----ECCHILMSVSKLQERRFIWAESFALRDGERLIC
hMannIIa_D55649 184 FERTQ-----ECCHILMSVSKLQERRFIWAESFALRDGERLIC
Mouse_MannII_[X] 183 FERTQ-----ECCHILMSVSKLQERRFIWAESFALRDGERLIC
hMannII 184 FERTQ-----ECCHILMSVSKLQERRFIWAESFALRDGERLIC
CionaMannII_[AR] 186 FERTQ-----ECCHILMSVSKLQERRFIWAESFALRDGERLIC
ArabMannII 171 FERTQ-----ECCHILMSVSKLQERRFIWAESFALRDGERLIC
Insect_MannIII 142 FERTQ-----ECCHILMSVSKLQERRFIWAESFALRDGERLIC
hLyso_MannII 80 VQGYGIXNDICAGVCFYDS-SALIAETRELVTAESLROTHATQEVV
hCyto_MannII_[N] 146 VEVACH-----GLLGAGAGSM AAPPDRIQVLSRAEAVRDUVBMFLVDIELLG
```

Droso\_MammII\_[X 214  
C.elegans\_MammI 249  
rMammII\_DCM\_218 329  
hMammIIa\_D55649 236  
Mouse\_MammII\_[X 235  
hMammII 236  
CionaMammII\_[AR 238  
ArabMammII 223  
Insect\_MamIII 194  
hlyso\_MammII 140  
hCyto\_MammII\_[W 198

Droso\_MammII\_[X 270  
C.elegans\_MammI 307  
rMammII\_DCM\_218 375  
hMammIIa\_D55649 292  
Mouse\_MammII\_[X 291  
hMammII 292  
CionaMammII\_[AR 294  
ArabMammII 279  
Insect\_MamIII 250  
hlyso\_MammII 198  
hCyto\_MammII\_[W 257

Droso\_MammII\_[X 330  
C.elegans\_MammI 367  
rMammII\_DCM\_218 435  
hMammIIa\_D55649 352  
Mouse\_MammII\_[X 351  
hMammII 352  
CionaMammII\_[AR 354  
ArabMammII 339  
Insect\_MamIII 309  
hlyso\_MammII 252  
hCyto\_MammII\_[W 313

Droso\_MammII\_[X 389  
C.elegans\_MammI 426  
rMammII\_DCM\_218 494  
hMammIIa\_D55649 411  
Mouse\_MammII\_[X 410  
hMammII 411  
CionaMammII\_[AR 413  
ArabMammII 399  
Insect\_MamIII 366  
hlyso\_MammII 303  
hCyto\_MammII\_[W 373

Droso\_MammII\_[X 448  
C.elegans\_MammI 485  
rMammII\_DCM\_218 553  
hMammIIa\_D55649 470  
Mouse\_MammII\_[X 469  
hMammII 470  
CionaMammII\_[AR 472  
ArabMammII 458  
Insect\_MamIII 426  
hlyso\_MammII 361  
hCyto\_MammII\_[W 433

Droso\_MammII\_[X 492  
C.elegans\_MammI 529  
rMammII\_DCM\_218 601  
hMammIIa\_D55649 518  
Mouse\_MammII\_[X 517  
hMammII 518  
CionaMammII\_[AR 515  
ArabMammII 514  
Insect\_MamIII 470  
hlyso\_MammII 401  
hCyto\_MammII\_[W 474

Droso\_MammII\_[X 537  
C.elegans\_MammI 578  
rMammII\_DCM\_218 655  
hMammIIa\_D55649 572  
Mouse\_MammII\_[X 571  
hMammII 572  
CionaMammII\_[AR 569  
ArabMammII 567  
Insect\_MamIII 530  
hlyso\_MammII 448  
hCyto\_MammII\_[W 523

Droso\_MammII\_[X 594  
C.elegans\_MammI 628

Page 4

```

Mouse_MannII_[X 986 -----SPVGYPSILGDMTSSTFDRRPLPTVGG
hMannII 985 -----S-VGYPSILGDMTSSTFDRRPLPTVGG
CionaMannII_[AK 990 -----AKIAYPSILAVYQ65NHTIRPFGNG
ArabMannII 989 -----MPRPSILSHICADRYCINTFIAR
Insect_MannIII 956 -----SMPGSTRARDTSRPGFVVRNRRPGQQRSPYQVSTADYLSRMFYENUYLDT
hLyso_MannII 843 -----VLDTAQAAAGHR-----IAAQETLACVADPGG
hCyto_MannII_[W 916 -----QDAGVQAAYSLH-----TDLALPAPSPAPATSWAFSS
Droso_MannII_[X 1000 -----NEWIGAGG-----PGGDEIAREDDISVRRITFS
C.elegans_MannI 1027 -----TPKISSIK-----MORRCHCHITPTLASPTTY
rMannII_OCM_218 1126 -----RSTSEPTER-----SRPLASPPCPHLDLRLPARVSVPRANPRQAPCLIGRAAD
hMannIIa_D55649 1020 -----NQLPGPCR-----SRPLASPPCPHLDLRLPARVSVPRANPRQAPCLIGRAAD
Mouse_MannII_[X 1027 -----QLPSPAYKLLSEPIQSSPPCPHLDLRLPARVSVPRANPRQAPCLIGRAAD
hMannII 1023 -----KYSSPTLKLOGSPLOSPCPHLDLRLPARVSVPRANPRQAPCLIGRAAD
CionaMannII_[AK 1032 -----PVLHEDRSPPMPCHHLDLRLPARVSVPRANPRQAPCLIGRAAD
ArabMannII 1029 -----PQDISVVPQYGSAPLAPRACHHLDLRLPARVSVPRANPRQAPCLIGRAAD
Insect_MannIII 1016 -----SEVGEIRKP-----QSYLQSPHPPGHIPTIRKEDDVLE
hLyso_MannII 875 -----GAAYHLGAPPRTPSGPRRDPSPHPTDAWGPENVLL
hCyto_MannII_[W 953 -----PAVVLITK-----QATSSPQREHVLVLYAH
Droso_MannII_[X 1032 -----SARTORVYCHERTNLAGCTPHEHTQELDVCHLLPNVARCERTTYL
C.elegans_MannI 1059 -----KANKERTYKKAAMVMREVPCR-SRLTLPDTSCLATGLEIPKI
rMannII_OCM_218 1183 -----PPPLLSLTVPQDTLPAADANLHNEPCCRSEANLGPNCITQGRVALGSLFPGDIL
hMannIIa_D55649 1056 -----DTLPARTALHNRGHCSEANLGPNCITQGRVALGSLFPGDIL
Mouse_MannII_[X 1066 -----KGYDEALILHRCGCOFSGGGLPCITQGRMVLGLFMAFHE
hMannII 1060 -----NGHNEALILHRCGCOFSGGGLPCITQGRILVQLLMFIFHE
CionaMannII_[AK 1064 -----VAPDQSLILHRCGCOFSGGGLPCITQGRILVQLLMFIFHE
ArabMannII 1065 -----QQLHEDKPRFALHRCGCOFSGGGLPCITQGRILVQLLMFIFHE
Insect_MannIII 1052 -----LPPHRSYVLRPCGSCVGEIPVARSAPSKRTFNGLNICHTAV
hLyso_MannII 916 -----LRECPAVERDSGRILAPVTNLDPSFTYIRLQTTTLVANGLERAA
hCyto_MannII_[W 981 -----GRVDCWHLSLPVCELCILRRDPAGELTAGQPPHRLFS
Droso_MannII_[X 1081 -----CMRHLDGMAPEVCPMS-----TAYSSG66
C.elegans_MannI 1107 -----STKSAKRESSTNLYEGN-----KARQPRCEMISITISY
rMannII_OCM_218 1243 -----F-LPPSILSLYPLASPS-----WSTDYLSMEIAGLRLG
hMannIIa_D55649 1103 -----F-LPPSILSLYPLASPS-----WSTDYLSMEIAGLRLG
Mouse_MannII_[X 1112 -----S-LVPSTSLMRSPPDAQ-----HNSRSLSPMEISELRLNT
hMannII 1108 -----S-LVPSTSLMRSPPDAQ-----HNSRSLSPMEISELRLNT
CionaMannII_[AK 1112 -----S-LVPSTSLMRSPPDAQ-----HNSRSLSPMEISELRLNT
ArabMannII 1119 -----S-LVPSTSLMRSPPDAQ-----HNSRSLSPMEISELRLNT
Insect_MannIII 1100 -----S-LVPSTSLMRSPPDAQ-----HNSRSLSPMEISELRLNT
hLyso_MannII 965 -----S-LVPSTSLMRSPPDAQ-----HNSRSLSPMEISELRLNT
hCyto_MannII_[W 1027 -----S-LVPSTSLMRSPPDAQ-----HNSRSLSPMEISELRLNT
  
```

Return Help Report Bugs

## Citation

### Algorithm Citation:

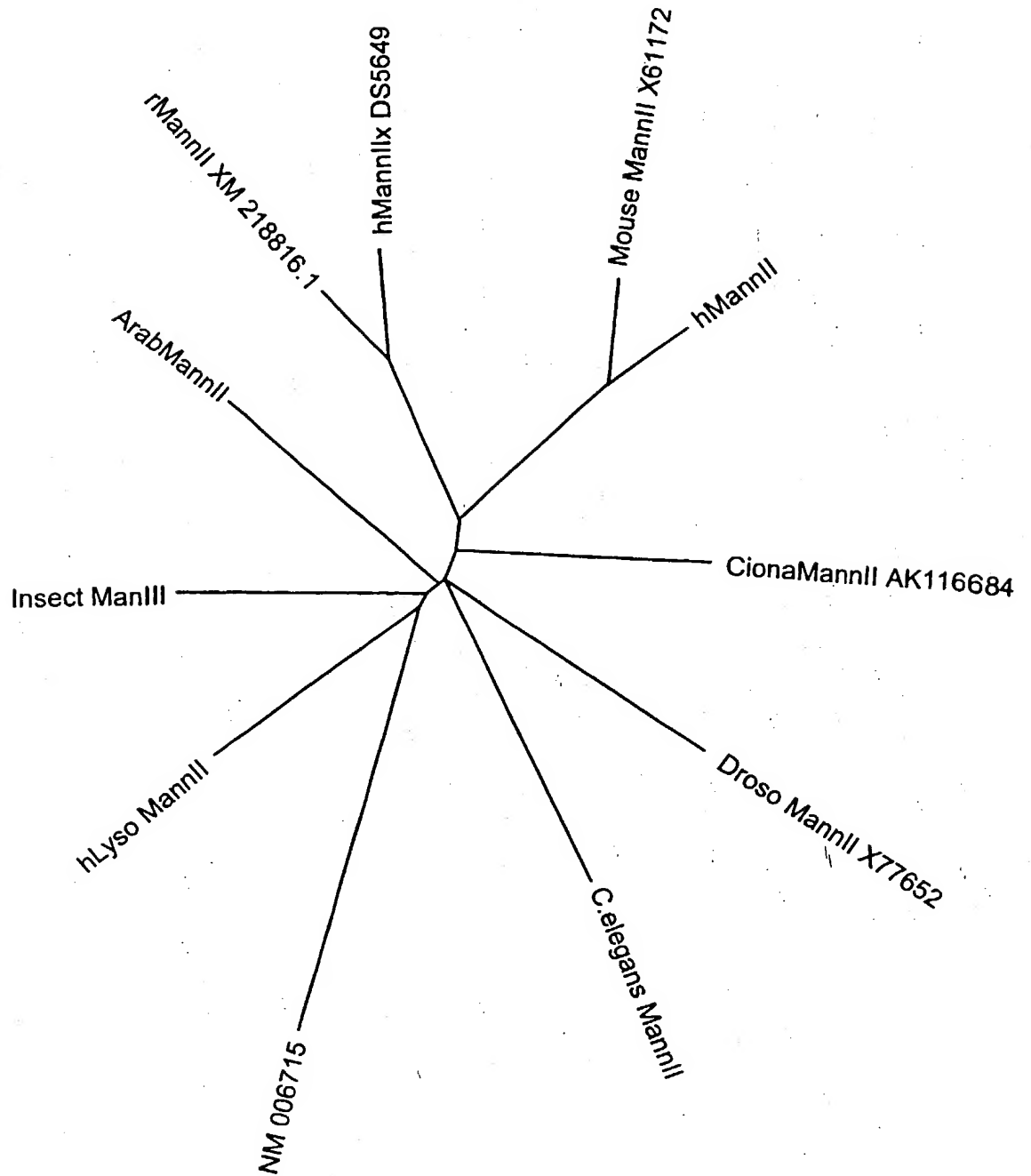
Not given, but presumably Kay Hofmann and Michael D. Baron.

### Program Citation:

Boxshade version 3.3.1, by Kay Hofmann and Michael D. Baron.



FIG. 24



**Arabidopsis thaliana Mannosidase II (NM\_121499)**

1 ATCCGCTTCTCTCGTATATCGGCAACAGCCGCGCTAGCTCCACGGCGGAGGAACCGCGGCTTGGGGCCACTCTCTCTTCCAAACAGCGTTATCAAGGTCAAAACTAG  
110 M P P F S S S Y I G N S R R S T G G G T G G W G Q S L L P T A L S K S K L  
37 A I N R K P R K R T L V N F I F A N F V I A L T V S L F F L T L F  
219 CCACCTCGCGCTCCAGGACGCGATCTCTCAGCATCTCTTACCTCAGATCCAATCGGATCGTCAAGCCAGGAAGAATTAATCGCGACCTTAAACGATTCCAAT  
73 H F G V P G P I S S R F L T S R S N R I V K P R K N I N R P L N D S N  
328 TCAGGCGCGCTCGTTGATACACAATCAAGATCTATACGATAGGATGGAGTTTGTATACAGATGGTGGTCCATGGAACAGGCTGGAGAGTACGTATAAAGACG  
110 S G A V V D I T T K D L Y D R I E F L O T D G G P W K Q G W R V T Y K D  
437 ATGATGGGAGAGAAGAGCTCAAAATCTTCGTGTCTCATTCTCATACGATCTCGTGGTGAAGATTGACTGTAGAGAGTATTATCAGAGACAATCCAGACATAT  
146 D E W E K E K L K I F V P H S H N D P G W K L T V E E Y Y Q R Q S R H I  
546 TCTGACACCATTTGTGAGACTTTATCAAGGATTCAGGAAGAAGTTTATATGGGAGGAGATGTCATATCGGAGAGATGGTGGAGAGACGCTTCCACCTAATAAACA  
182 L D T I V E T L S K D S R R K F I W E M S Y L E R W R D A S P N K Q  
655 GAAGCTTGACTAAATTTGGTAAAGATGGGACGCTAGAGATTTGGAGGTGGCTGGGTTATGAATGATGAGGCTAATTCACATTTTATGCCAATTTGAACAGATAG  
219 E A L T K L V K D G Q L E I V G G W V M N D E A N S H Y F A I E Q I  
764 CAGAGGGTAAATATGGCTGAATGACACAATTTGGGTTATCTTAAGAATTTCTGGGCTATAGATCCCTTTGGCTATTTCATCAACCATGGCTTATCTCTCGCGGTAT  
255 A E G N M W L N D T I G V I P K N S W A I D P F G Y S S T M A Y L L R R M  
873 GGGTTTGTAAACATGCTTTATTCAGAGGACTCATTACGAGCTCAAGAAAGACCTTCCCGCAGCATAGAATCTTGAATATATTGGCGTCAGAGCTGGGATGCTATGGAA  
291 G F E N M L I Q R T H Y E L K D L A Q H K N L E Y I W R Q S W D A M E  
982 ACCACGAGATCTTTGTCATATGATGCGGTTTATTATCATAGATATCCCAACACTTGTGGACGAGGCTGCAATTTGCTGTACGTTTATTTCGCTCGGATCGGGG  
328 T T T A T I F V H M M P F Y S D I P T C G P E A I C C Q F D F A R M R  
1091 GATTTAAGTATCAACTTTGCTATCGGGAAGACCCAGTGGAGACACATAGAAAATGTGCAGGAGAGGCTATTAAAGCTTCTGGATCAATCAGCAAAAATAATCCAC  
364 G F K Y E L C P W G K H P V E T T L E N V Q E R A L K L L D Q Y R K K S T  
1200 TCTATATCGAACTAATACACTTCTTATACCTCTTGGAGATGATTTTAGTACATTAGTATCGATGAGACCGAGGCTCAGTTCCGTAACCTACCATGATTTGTTTGTATC  
400 L Y R T N T L L I P L G D D F R Y I S I D E A E A Q F R N Y Q M L F D H  
1309 ATCAACTCTAATCTAGTCTAAACCGCAGGAACAAAGTTTGGTCAATTTGGAGGATTTATTCAGAACAGTCCGAGAGAAGCAGACAGAGTGAATTTATCTCGCTGGTG  
437 I N S N P T S L N A E A K F G T L E D Y F R T V R E E A D R V N Y S R P G  
1418 AGGTGGCTCTGCTCAGGTGTGTGGTTTCCCTCTCTGTCAGGTGACTCTTTACATATCGAGATAGGCAACAGACTATTGGAGTGGTTATTATGTTTCAAGACCTTT  
473 E V G S Q Q V V G F P S L S G D F F T Y A D R Q Q D Y W S G Y Y V S R P F  
1527 CTTCAGAGCTGTGATCGTGCTCGAGCATACCCCTCGTGGAGCTGAGATCATGATGTCATTCTGCTAGGTTTATGCCATCGAATCAATGTGGAGAAATTTCCAACA  
509 F K A V D R L E H T L R G A E I M M S F L L G Y C H R I Q C E K F P T  
1636 AGTTTATCGTAAAGTTGACTGCTCAAGAAGAAATCTGGGCTTTTCCAGCAACCATGATGGGTAACTGGAACCTGCTAAGGATTATGTGGTACAAGATTACCGGCCACC  
546 S F T Y K L T A A R R N L A L F Q H H D G V T G T A K D Y V V D Y G T  
1745 GGATGCACTACTTCAATGCAAGACTTCAGATCTTTATGTCATAAGCAATCGAAGTTCTTCTGGGATCCGCGCAGAGAAAGAAAATCTGATCAATCCCATCACTTTT  
582 R M H T S L Q D L Q I F M S K A I E V T L L G I R H E K E K S D Q S P S F F  
1854 CGAGGCGAGCAATAGATCAAGATATGATGCTCGGCCAGTTCACAAGCAATTTGCTGCCGGGAGGAAGAAATCCGACACAGTATTACTCTTCAATCCGAGCAAGAC  
618 E A E Q M R S K Y D A R P V H K P I A A R E G N S H T V I L F N P S E Q  
1963 ACAGAGAGGAGGTTGTGACGGTGTGTTTAAACCGCGCTGAATCTCGGTTTGGACCTAACTGGACTGTGTCCCTAGCCAAATTTCTCCTGAAGTCAGCATGAGC  
655 T R E E V T V V V N R A E I S V L D S N W T C V P S Q I S P E V Q H D  
2072 ATACCAAACTATTACCCGCGACATCCGCTTTACTGGAAGAGCTTCCATCCCAAGCTCTGTGCTCGAGAACATATTTCATGCTAATGGGAATCTCGAGTGTGAGAAAGC  
691 D T K L F T G R H R L Y W K A S I P A L G L R T Y F I A N G N V E C K A  
2181 TACTCGCTCAAACTCAAATCGCTCTGAGTTTGACCCATTCTCTGTCTCCATATCTCTGCTCCAACTCGGACACAGCGCTTACTGAGATCCGAATGAACAT  
727 T P S K L K Y A S E F D P F C P P P Y S C S K L D N D V T E I R N E H  
2290 CAGACTCTTGTGTTTGATGTGAAGAACGGATCACTCGGGAAGATAGTCCATAGAAACGGATCAGAGACTGTGTGGGAGAAGACATAGGTATGTACTCTAGTCAGAGA  
764 Q T L V F D V K G S L R K I V H R N G S E T V T V G E E I G M Y S P E  
2399 GTGGAGCTTACCTGTTCAAACGAGGATGGTGAAGCTCAGCCAAATGTTCAACCTGATGGACATGTAGTACCTCTGAGGCGTCTGCTGGTTCAAGAAGTCTTCTCTTACC  
800 S G A Y L L F K P D G E A Q P I V O P D G H V V T S E G L L V Q E V F S Y P  
2508 TAAACCAAAATGGGAGAAATCACCCCTCTTCAGAAACTCGTCTTACATCGAGGATTAACAGCTTCAGGATCAAGTGGCTGAGATAGAATATCATGTTAGCTTCTCT  
836 K T K W E K S P L S Q K T R L Y T G G N T L Q D Q V E I E Y H V E L L  
2617 GGTAATGATTTGATGACCGGGAATGATTTCCGGTACAAGACTGATGTTGACACAAGAAGGTGTTCTATTGAGATCTCAATGGTTTCAAATGAGCAGGAGAGAAA  
873 G N D F D R E L I V R Y K T D V D N K K V F Y S D L N G F O M S R R E  
2726 CTTATGATAAGATCCCTCTCAAGGAACTACTACCAATGCCATCTCTCGATTATTCCAAGGATCCAATGGTCAGAGATCTCCGTGCACCTCTCGTCAATCTCTCGG  
909 T Y D K I P L Q G N Y Y P M P S L A F I Q G S N Q R F S V H S R Q S L G  
2835 TGTTCGACGCTCAAGAGGGGTGGTTGGAGATTATGCTGCAGACAGCGTTGGTTGCTGATGACGACGGGGTCTAGGCAAGAGTGTGATGGATAACCCGCGCAATGACC  
945 V A S L K E G W L E I M L D R L R L V R D D G R L G Q G V M D N R A M T  
2944 CTGGTATTTCACCTTCTCGCGAATCAACATTTCTCAAGCAGACCTCGTCCCAACATACCCCGAGGAACCTTCGCTCTCTCTCACTCATAGGTGCTCACTTAA  
982 V V F H L L A E S N I S Q A D P A S N T N P R N P S L L S H L I G A H L  
3053 ACTACCCCATAAACACATTATCGCAAGAAGCCGCAAGACATATCTGTGGCTGTTCCACAATACGGTTCTCTTGTCTTTCAGCCAAACCGTTACCATGTGACCTCCA  
1018 N Y P I N T F I A K K P Q D I S V R V P Q Y G S F A P L A L P C D L H  
3162 CATTTGAATTTCAAGGTTCTCGTCACTCAAAATCTTCAGCAATTTGGAAGAAGCAAGGCTGCTGCTTATCTCAATAGACGAGCTTGGGATTCAGCTTAT  
1054 I V N F K V P R P C S A G C T S Y S Q L L E E D K P R F A L I L N R R A W D S A Y  
3271 TGGCATAAAGGAAGACAGTAATTCGCAACAGCTGGCTAATGAACAGGTAATCTTCCGACATGTTCAAAGATCTTGACGTTCAAAGGTAAACCAACTCACTGA  
1091 C H T K G R Q V N C T S M A N E P V N F S D M F K D L A A S K V K P T S L  
3380 ATCTCTTCAAGAAGATATGGAGATTCTTGGGTACGATCAACCAAGCTACTCGAGATAGTTCACAGCCAGGGAAGACGTGTCTCGATCTCTCCATCGGAATACG  
1127 N L L Q E D M E I L G Y D D Q E L P R D S S Q P R E G R V S S P M E I R  
3489 AGCTTAAAGCTTGAACCTGCGACCTCAAGATGA  
1163 A Y K L E L R P H K

FIG. 26

*C. elegans* Mannosidase II (NM\_073594)

```
1 ATGGCAAAACGCAATTTCTATATTCTATGTTTGGGAGTCTTCTCACCGTATCACTCTATTGTACAAATGGAATGAAACCGGAGCTGAAGCGCTCACCAAAACGACA
1 M G K R N F Y I I L C L G V F L T V S L Y L Y N G I E T G A E A L T K R Q
111 AGCAAAATGATTACGGCGGAAATCGGAAATTTGGAGCATGTAGCAGAAGAAATGGAAGAACGATAGACCGCTTGAACACGAAGTTCAACGAGCAAAAGCTGAAAAAT
37 A N D L R R K I G N L E H V A E N G R T I D R L E Q E V Q R A K A E K
221 CGGTAGATTTTATGATGAAGAAAAGAAAAACGGAAGAAAAAGAGTAGAAAAAGAGGAAAAAGAGTTGCACCGATTCCAGTTCCGAGGAATCTGGTGAATGGCTCAT
74 S V D F D E E K E K E V E K E E K E V A P V P V R G N R G E M A H
331 ATTCATCAAGTAAAGCAACATATCAAGCCAATCCATCGATGAAAGATGTTTGTGGATTAGAGAAAACGTCAGCATTGCTCATTGAGACCTGCAGATGCTCGATCTCTA
111 I H Q V K Q H I K P T P S M K D V G G I R E N V S I A H S D L Q M L D L Y
441 TGACACCTGGAAGTTGGAATCCAGACGGAGGTGTATGGAAACAAAGATGGAATTTGAATACGATCGACAGAAAATCAATCTCTTCCACGTTTGGAGCTATTGTGA
147 D T W K F E N P D G G V W K Q G W K I E Y D A E K V K S L P R L E V I V
551 TACCTCATTTCTATTGTGATCCGGATGGATTGACTTTTGAAGAGTATTACAACAGACAACTCGCAATATTCTTGATGGAATGGCTAAACATTTGGCAGAAAAAGAC
184 I P H S H C D P G W I M T F E E Y Y N R Q T R N I L D G M A K H L A E K D
661 GAAATCGCGTTTATATATGCAAGAAATATCAATTTTGAAGCTTGTGGAGAGACAGGATGAAATTAAGAAAGATTAAGGATTTTGAAGCAGGAAAGTTGA
221 E M R F I Y A E I S F F E T W W R D Q A D E I K K K V K G Y L E A G K F E
771 AATTGTTACTGGCGGATGGTTATGACAGATGAAGCTAATGCACATTATCACTCAATGATCACTGAATTTGTCGAAGGACATGAATGGATTCAAAATCAITTTGGGAAAA
257 I V T G G W V M T D E A N A H Y H S M I T E L F E G H E W I Q N H L G K
881 GCGCAATCCCAATCTCATTGGTCAATGATCCATTCGGTTTATCACCATCAATGCCACATCTTCAACTTCTGCTAATTAACCAATGCTGTAATCAAGAGATTCAT
294 S A I P V K Q S H W S I D P F G L S P S M P H L L T S A N I T A N I T A N I V I Q R V H
991 TATTCGGTGAACGTCAGCTTGTCTGAAAAAGAACTTTGAATTTCTACTGGAGACAATTTTGGATCACTGGACATCTGATCTTGGTTCACATAATATGCTCTTCTA
331 Y S V K R E L A L K K N L E F Y W R Q L F G S T G H P D L R S H I M P F Y
1101 CTCTTACGATATACCTCATACGTGTGGCCGAGAACCTGTGTTTCTGTCAATTCGATTTCCTGATGAATGCCAGAAAGTGGAAAAATCATGTGATGGGAATCCCTCCAC
367 S Y D I P H T C G G P E P S V C C Q F D F R R M P E G G K S C D W G I P
1211 AGAAAAATTAACGTCACAATGTGGCTCAGAGAGCTGAAATGATTATGATCAATATAGAGAAAAAGTCAACTTTTCAAGAAATATGATTTTCAACCAATTTGAGAT
404 Q K I N D D N V A H R A E M I Y D Q Y R K K S Q L F K N N V I F Q P L G D
1321 GATTTCAGGTACGACATTGATTTTGAATGGAATTCACAATATGAAGAAATTTGTCGAATACATGAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGA
441 D F R Y D I D F E W N S Q Y E N Y K K L F E Y M N S K S E W N V H A Q F G
1431 AACTCTTTCTGATTATTTCAAGAGCTTGATCTGCAATTTCTGGCTTCTGGGAGCACTTCAACTTTTCTGGAGATTCTTCACTTATGCGGACAGAGATGATCAT
477 T L S D Y F K K L D T A I S A S G E Q L P T F S G D F T Y A D R D H
1541 ATTTGAGTGATGACTTCACTTCCGCTCCATTCTATAACAGCTTGATCGGGTTTCCCAACTATTTTAAGATCAGCTGAAATCGCCTTACCCTTGCAGAAATTTGAAGAA
514 Y W S G Y F T S R P F Y K Q L D R V L Q H Y L R S A E I A F T L A N I E
1651 GAAGGAATGGTTGAAGCGAAAAATTTTGAAGAGCTTGTGACTGCTCGACGAGCTCTTCACTTTTCCAACATCAGCATGGTGTAACTGGTACGGCAAAAGATCAGCTGT
551 E G M V E A K I F E K L V T A R R A L S L F Q H H D G V T G T A K D H V
1761 CTGGATTATGGTCAGAAAATGATTGATGCTTTGAACGATGTGAGGATATCTTTTGGAGAGCTCTTGTGATTGCTGGGAATTTGATCAAGCAATTAAGATGCAAGTG
587 L D Y G Q K M I D A L N A C E D I L S E A L V L L G I D S T N K M Q M
1871 ATGAGCATAGATTAAATGAAGAACTTACCGGAAAAAGTGTCTATAAAATTTGGGCAAAACGTCGATTGTTCAATACCTTATCTAGAAATCGCAACGAGCAATTTGT
624 D E H R V N E N L L P E K R V Y K I G Q N V V L F N T L S R N R N E P I C
1981 ATTCAGTTGATTCTTTCAGCTGGTGTGCAAGCTGATCTCCCAATTAAGAAACCAAGTTTCGCGGTTTATGATATGATGAAGAGAAGAAACGCTTGTGTCAA
661 I Q V D S L D A G V E A D P P I K K Q Q V S P V I A Y D E E K K T L V V K
2091 AAACGGAATATTGCAACTTTGCTTCATGTTATCACTTGGACCAATGGAGCTGTGCTGATTTGAGATTTGATGAAATACAAACATCCAAAGTTGAAATATCAACCAATA
697 N G I F E L C F M L S L G P M E S V S F R L V K N T T T S K V E I I T N
2201 ATGCGGCAGAAATCAAGAAACAGTTTAAATCTTCATCCACTTCTGGAGACTTACTGTGAAACACGACAAAGTTGAAGCTGAATTTGATGGGAGAAATGGAATGATT
734 N A A E F K E T S F K S S T S G D F T V K N D K V E A F D G E N G M I
2311 AAAAGAGCTACCACTTGTGATGATAACCAATTTGATTGATTTCACTTATTCATTATGAGGACCGGAAGTCAAGAGAAAGTTCCGAAATGGAATGAAGACAA
771 K R A T S L V D D K P I D L N S H F I H Y G A R K S K R K F A N G N E D N
2421 CCCGGCTGGCGCATACCTGTTCTTCCGATGGAGAAGCTAGAGAACTCAAAAAACAACTCAAGTATTGGATATTGGTAAAAGGAGAAGTTGTTCAAAAAGTTGTTGCAA
807 P A G A Y L F L P D G E A R E L K K Q S S D W I L V K G E V V Q K V F A
2531 CTCGCAACATGATCTGAAATATTGCAACGTCACACATTTATCAAGGCTTCCATGGATTGATTGGAATATGAAGTTGATGTACGTTCCAGGAGAAATTCGAGTTG
844 T P N N D L K I L Q T Y T L Y Q G L P W I D L D N E V D V R S K E N F E L
2641 GCATCGAGATTCAGTTCTTCAGTAATAGTGTGATGAGTTTTCAGTCAATGGAATGCAATGATAAAAGGAGACGACAACTAAATACCAACACAGGCGAA
881 A L R F S S S V N S G D E F F T D L N G M Q M I K R R R T K L P T Q A N
2751 TTTCTCCATGCTGCTGGTGTTTTACATTGAAGACGATACCAAGATGCAATTCATTCGGCACAGGCTCTCGGAGTTAGCAGCTCTCTGCTGGGACAAATTTGAAA
917 F Y P M S A G V Y I E D D T T R M S I H S A Q A L G V S S L S G Q I E
2861 TAATGCTTGATCGAGACTTAGTTCAGATGACAAACAGAGGCTCTTCAGCAAGGAGTTAGAGACAAACAAACAGAGTTGCACATTTCCGTATTCTTATTGAGCCGATGCT
954 I M L D R R L S S D D N R G L Q Q G V R D N K R T V A H F R I V I E P M S
2971 TCATCGAGTGGTAAATAAGAAAGGAAGACGAGTTGGATTCCATTACATGTTGGTCACTCGCTACGTTGGTCTCTTCATTATCTCTTGTCAAAATGATTGGAGATGCAAC
991 S S S G N K K E E R V G F H S H V G H L A T W S L H Y P L V K M I G D A T
3081 ACCAAAATCTATTTTTCGAAAAATGTGAACAAGAGCTGAAGTGTGACCTGATCTAGTGACATTTAGAACACTGGCATCGCGGACAACTACGAGCAACGCAAGAT
1027 P K S I S S K N V E O E L N C D L H L V T F R T L A S P T T Y E A N E R
3191 CTACGGCAGCTGAGAGAAAGCAGCGATGGTGTGATGATAGATGTTTCCAGACTGTAGATCCAGGCTTACCTCCAGACACGTCATGCTTAGCTACTGATAGAAAT
1064 S T A A E K K A A M V M H R V V P D C R S R L T L P D T L E I
3301 GAGCCACTCAATTTGATCTCGACACTGAAGTCTCGAAAAAACGCTCACTAACCAATCTTTATGAAGGAAACAGGCTGAACAAATCCGACTCCAACCAACGATATTC
1101 E P L K L I S T L K S A K K T S L T N L Y E G N K A E Q F R L Q P N D I S
3411 CAGTATTCTGTATCATTTTAA
1137 S I L V S F
```

***Ciona intestinalis* mannosidase II (AK116684)**

1 ATGAAGCTCAAACGCCAGTCTCTATTCTTTGGTGGAAATCTGTTCTTCGGGAGTATCTGGTTATGATAGGTCAACTTGACACTCCTAATTGCCGCAGAAAGTCAAAT  
3 M T C K L R Q F L F F G G I L F F G S I W F M I G Q L D T P N S P Q K V K  
110 TCTCGGAAGCAGTGAAAATGACCAAGTTCGAACCTTCAAGACAACCTTAGTCTGGTGGAAAAAGAAATGTTAGAAAATCGTAAAAATGACACAGGTGAAAGATAG  
37 F S E G S E N D Q V R T L O D K L S L V E K E L L E N R K I M H K V K V  
219 TCTACAGGATATGACACCATGAAAAATTTGATGCGCTATGACCGCGGAGAAATAGAAACAACGCTCAATAAACCTGTGCTACCACTTAATGAGTCCCAAGCAATTT  
73 L Q D M T P M K N V H V P M Q R G E I R N N V N K P V L P L I M P K Q F  
328 GCGAATGACTCCCGAATGAGTGACACGTGTCTGTCTGCTACTCCGTGCGCAAGTCCGATGTAACATGATTAACTGTATGATCATCTCCATTGTGATGATCCAG  
110 A N D S R M S D T C P V L S Y S G G K S D V N M I N V Y D H L P F D D P  
437 ATGGTGGAGTTTGGAAACAAGGTGGGACATCCGACATCGGATCAGGAATGGCTGGGAGAAAATGAAAGTGTTCTATTGCTCCCTACATCAATGATCTGGTGGT  
146 D G V V K Q G W D I Q T S D Q E W A G R K L K V F I V P H S H N D P G W  
546 GTTAAAGACGGTGGAAAGATATCTCAGCGATCAAAACAACATTTCTCAATAATTTGGTGGATCTTTGAGTGACAGACCTCGCAAGCAAGTTTATCTGGGACAGAGAT  
182 L K T V T E R Y F S D Q T Q H I L N N I V D A L S Q D P A R K F I A W E M  
655 TCGTATCTCTCAATGTGGTGGGACATGCCACACCTGATCGTAAGCAGAAAAATGCAGACACTCGTGAAGAATGGACAGCTTGAGATAGTTACGGGTGGTGGGTCTATCA  
219 S Y L S M W D I A T P D R K Q K M Q T L V K N G Q L E I V T G W V M  
764 ATGATGAAGCAAACTCATTTCTGATGATGATCAACTATTGAAGTATGGAATGGTGGAGGCAACATGGAATGTTGTTCCAAAAAGTGGGTGGGCGATGA  
255 N D E A N T H Y F A M I D Q L I E G M E W L R T L N V P V P K S G W A I D  
873 TCCCTTGGTACACCCCAATGGCTTATATCTGAAACAGATGAAGTTCAAAACATGCTGATACAAAGATCCATTATGCAGTGAAGAAGTATCTTGCTCAGAA  
291 P F F G H T P T M A Y I L K Q M K F K N M L I Q R V H Y A V K K Y L A Q E  
982 AAGTCTCTGGAATTCAGATGGAGACAAATGTGGGATTACGTTCAAGTCAGACATGATGTGCTCATCTGATGCTTCTATTCTATGATGTCTCTCACTACTTGTGGCC  
328 K S L E F R W R Q M W D S A S S T D M M C H L M P F Y S Y D V P H T C G  
1091 CAGACCCCAAGATTTGCTGCGAGTTTGATTTGCTGCGTTACCCGGGCGAGTAACCTGCCCATGGAAGTCTCTCTGTTGCCATCACTGACTCCAATGTAGAAAC  
364 P D P K I C C Q F D A R L P G G K I A T C T P W K V P P V A I T D S N V E T  
1200 ACGAGCCGAATACTACTTGACCAATATAGAAAAAGTCAAAACTCTTCAAAGTACACCCCTGCTTATTATATTAGGAGATGATTTTCGTTATTCTGCTGAGCAAGGAA  
400 R A G I L D Q Y R K K S K L F K S D T I L I L G D F R Y S L S K E  
1309 ACCAAGCATCAGTTTGACAACATCGCTCGAATTTCTCGTATGTGAATTCCGACCCAGAGTTTAAACGCCAAAACCTTCAGTTTGGAACTATTCCGAATATTTTGTAGCCA  
437 T N D O F D N Y A R I I S S N S H P E L N A K L O F G T L S E Y F D A  
1418 TGAATATCTGAAGTGGGGGAGAGGAAAACTCCACGTTTAAAGTGGTATTTCTTCACTTATGCTGATAGAGAAGATCACTATTGGAGTGGTACTACACTCAGCGCC  
473 M K S E V G G E E K L P A L S G D F F T Y A D R E D H Y W S G Y Y T S R P  
1527 TACCAACAAAATCGAGGAGAGAGCTCTGGAAAGCCACCTTCGAGGAGCAGAAATGTTGTTGCGCTCTCATGGCCCAAATCCAGTGGACAGGAGTTGGTGAACACTT  
509 Y H K M Q E R V L E S H L R G A E M L F A L S W P K I Q W T G L G E T F  
1636 TCACATGACACTTTACCACTGCTGCTGCTCAAGCAGCTCAAAATCTTGTTTGTGTTCAACACACAGTGGTATTAACAGGCACAGCAAGGATCATGTTGTTGTTGATTACG  
546 S H E L Y P L L V Q A R Q N L G L F Q H D G I T T G T A K D H V V D V  
1745 GGAATAAACTCATGAAGAGTGTTATGGATGCAAAAGAGTAAITTCATACAGTGCCCAAGTTCTGTTGCAAGAAGATGATCAGCTTTGATCCAAATACCATGGTACTTAA  
582 G N K L M K S V M A D A K K V I S Y S A Q V L L O E M I T F D P N T M V L N  
1854 CTATGATGAGGTGTATCAAGCTCAGAACCAACCACTCGCCCTGTGGTTGTTAAGCTACCAACAGAGARTGAAGAAGCGCGGAAAGTCTGTCTCTACAACCTCTCTGGAT  
618 Y D E V Y Q A Q N O Q P A P V V K L P T K N E E A R K V V L Y N S G D  
1963 TACGACAGAACTGGTGTCTGGCTGCTCAATTTGTTACGTCACCCGACGTTGGTGTGATGTCAGAAAAACAAAGCTCTGTTCCATCGCAACACAGTCCGATCTGGCTAGATT  
655 Y D R T G V V R L I V T S P D V V M S E N K N V P S Q T S P I W S D  
2072 CGACGGAAGATCCGACAGACAGTTTGAAGCTGGTTTTCTTTCACTGTGTCCCGGATAGGACTGGCGGTGTACAAGATATGGGAAGCAACGACGAGTACGACAGACAC  
691 S T E I R T D Q F E L V F L S T V P A I G L A V Y K I W E D N D V A D T T  
2181 GCACCTCAACTGTTAAGTTTATCAACCCGAGAGTTGGGTTTTGCAAGCAACCCGCAAGTAAAGTTGATCTGCAGCTTGAGGATACGGGGAGTTTACCATCATGAATGAC  
727 H S T V K F I N P R V G F S K R T R S K F L V D V E D S G E F T I M N D  
2290 CAATTAGTTGGCATTCTCTGGGCAAAACGGGATGCTGCGAGTCAGTCACCACTGTGGCTGACAACGTTAAAGCGCAAGCTCGGAATGAACTCGTGGCTTATCTCTCTC  
764 Q L V A H F S G Q N G M L Q V S V T T V R D N V K T Q L G I E F V A Y T S  
2399 GTAATAAGAAAGACAAGAGCGGCGCTTACTGTTGTTCTGCTGCTGGACAGCACAACCCGATGTAACAGAATCCACCGACCGTTAGTAAGGATCATCAGGGGTCAGT  
800 R N K K D K S G A Y L F L P A G P A Q P H V T E S H R L P V R I R G P V  
2508 GATGTCACCGGTGCATGTTCTACTACCGAAGTTCTGCATAAAGTACCCTATACACCGGATCTGGTGAGGACGACGAGCTTTTAGCGTCCAGCTCTCTAACGACGT  
836 M S T V H V L L P N V L H K V L T Y T G T G A G T Q S L G V H V S N D V  
2617 GACGTTAGAACTGGCTACGACAACAAGAACTCAGTATGAGGTTAAACAGCGAAGTTTATCGGGAAGCAAAATCTTTACGGAATTTAAACGGTTTCAAATTAACCCC  
873 D V R T G Y D N K E L S M R L N S E V L S G S K F F T D L N G F Q I Q P  
2726 GAACCACGTATTCTAAACTGCCACTACAAGCAAACTTACCCAAATACCCCAATGGCGTTTCATACAGACGAAAAATCAAGTAACTTTGATGACGGGCCCAACCACT  
909 R T T Y S K L P L Q A N F Y P I P T M A F I Q D E K S R L T L M T A Q P L  
2835 GGGTGTGCTCTCACTGAAGTCAGGTCAACTTGAGGTGGTTTGGATCGCGCTTTAATGCAGGACGACAACAGGGGGTGGGTCAAGGTGTGAAGATTAATTTACCACT  
945 G V A S L K S G Q L E V L D R L L M Q D D N R G V G G Q G V K D N L P T  
2944 CCTGAGAGTTTCTGATCATCTGCGAAAGATGGAACCGCTATTGCGACGAAAGAAAGCAATCGTCACCGAAGCTCGCGCTATCATCTATGCGTGTGATCATGATCAT  
982 P E S F V I M L E R W T A I A K E S K S A K L A Y P S M A V Y Q S S  
3053 GGGAAATGCTACCCCAATACGTCCTAATCGGTAATGGGCCGGTACATTTGAAGAAGATTAACGCTCGCTGCCACAGCTTTACCATGCGACGTGCACGTGTTAAA  
1018 W E L L H P I R P M S V N G P V H L K E D Y R S L P Q P L P C D V H V L N  
3162 CTTCGGAGCAATTCATTCTAAGAGTCAGTTGCCCTACCCGACCAATCGGCTGCTGTTCTACACACAGTTGGGGCGGAATGCTCTTGGACCGGTAAGTAAATTTACCA  
1054 L R A I H S K D A V A P T D Q S A L L L H T V G R E C S L D A D K Y F H  
3271 CCAAGTCGCTCATGACGGGCTCGAGAAATGGCTATCAGCATCTGACAGCTTTTACTAACTCTGGCATGGGAAGAGCTCGCTGCTCTTACAACACGACGGCTCGT  
1091 P T C L M H G V E K L A I T S T L T F T N S G M R K T S L S L O H D G S  
3380 TCGTGGACACCAAGGCGGTATACAGTTTCCCCAATGGAGATACAAGTTTACAAAATGACTGACGTAA  
1127 L L D N Q G G I T V S P M E I Q A Y K I V L T

FIG. 28

Drosophila mannosidase II (X77652)

```
1 ATGTTGCGAATACGTCGGCGGTTGCTTGGTAATTTGCTCCGGCTGCCTGCTGTTTTCTCAGCCTGTACATAATCTCAATTTTGGCGCGCGGCGAGCCACCAGA
101 M L R I R R R F A L V I C S G C L L V F L S L Y I I L N F A A P A A T Q
110 TAAAGCCCAACTGAGAACATTGAGAACAGCTGCATGAGCTGGAAATGGTTGACAGGACACGGGAGGAGATGCGGAATCTCAGGGCGGCTGTCGGCCAAACATC
119 I K P N Y E N I E N K L H E L E N G L Q E H G E E M R N L R A R L A K T S
128 CAATCGCGACGATCCAATAACACCTCCACTTAAAGTGGCTCGTTCGCCGAGGCGAGGCGAATGCCAAGATGTGGTCCAAGACGTCGCCAATGTGGATGTACAGATGCTG
137 N R D D P I R P P L K V A R S P R P G Q C Q D V V Q D V P N V D V Q M L
146 GAGCTATACGATCGCATGTCTTCAAGGACATAGATGGAGGCGTGGAAACAGGGCTGGAACATTAACTACGATCCACTGAAGTACACGCCCATCACAACTAAAG
155 E L Y D R M S F K D I D G G V W K O G W N I K Y D P L K Y N A H H K L K
164 TCTTCGTTGTGCGGCACTCGCACACGATCCTGGATGGATTGAGACGTTGAGGAATACTACGACGACACCAAGCACATCTGTCCAATGCATACCGCATCTGCA
173 V F V V P H S H N D P G W I Q T F E E Y Y Q H D T K H I L S N A L R H L H
182 CGACCAATCCCGAGATGAAGTTCAATCTGGCGGAAATCTCCTACTTGTCTCGGTTCTATCAGGATTGGGAGAGAACAAAAGCTGCAGATGAAGTCCATTGTAAAGAT
191 D N P E M K F I W A E I S Y F A R F Y H D L G E N K K L Q M K S I V K N
200 GGACAGTTGGAATTTGACTGGAGGATGGTAATGCCGACGAGGCGCACTCCCACTGGCGAAACGTAAGTCTGCTGACGTCGACCGAAGGCGAAACATGGTTGAAGCAAT
209 G Q L E F V T G G W V M P D E A N S H W R N V L L Q L T E G Q T W L K O
218 TCATGAATGTCACACCCACTGCTTCTGGGCCATCGATCCCTTCGGACACAGTCCCACTACATTTTGAGAGAGAGTGGTTTCAAGAATATGCTTATCQAAAG
227 F M N V T P T A S W A I D P F G H S T M P Y I L Q K S G F K N M L I Q R
236 GACCACTATTCTGTTAAGAAAGAACTGGCCCAACAGCGACAGCTTGAGTTCTGTCGGCCAGATCTGGGACAAACAAAGGGACACAGCTCTCTCACCACATGATG
245 T H Y S V K K E L A Q R Q L E F L W R Q I W D N K G D T A L F T H M M
254 CCCTCTACTCTACGACATTCTCATACCTGTGGTCCAGATCCCAAGGTTTGTCTGTCAGTTTCGATTTCAACGAATGGGCTCTCTCGGTTTGAAGTTGTCATGGAAGG
263 P F Y S Y D I P H T C G P D P K V C C Q F D F K R M G S F G L S C P W K
272 TGCGCGCGGTACAATCAGTGATCAAAATGTGGCAGCAGCTCAGATCTGCTGGTTGATCAGTGAAGAAGAAGGCGAGCTGTATCGCAACAACTGCTGCTGATTCC
281 V P P R T I S D Q N V A A R S D G L L V D Q W K K K A E L Y R T N V L L I P
290 GTTGGGTGACGATCTCGCTTCAAGCAGAACACCGAGTGGGATGTGACGCGCTGAACTACGAAAGCTGTTGCAACACATCAACAGCAGGCGCCACTTCAATGTCCAG
300 L G D D F R F K Q N T E W D V Q R V N Y E R L F E H I N S Q A H F N V Q
309 CGCGAGTTCGCGCACTGCAGGAATCTTTGATGCGAGTGCAACGCGGAAAGGGCGGCAAGCGGATTTCCACGCTGACCTTTTACATACGCGGATC
318 A Q F G T L Q E Y F D A V H Q A E R A G Q A E F P T L S G D F F T Y A D
327 GATCGGATAACTATTGGAGTGGCTACTACACATCCCGCCGTATCATAAGCGCATGGACCGGCTCCTGATGCATATGTACGTGCAGCAGAAATGCTTCCCGCTGGCA
336 R S D N Y W S G Y Y T S R P Y H K R M D R V L M H Y V R A A E M L S A W H
345 CTCCTGGGACGATGGCCCGCATCGAGGAAGCTCTGGAGCAGGCGCGCAGGAGGATGTCATTGTTCCAGCACCACGACGATATACTGGCAGCAGAAACCGCACGTA
354 S W D G M A R I E R L E Q A R R E L S L F Q H H D G I T G T A K T H V
363 GTCGTCGATACGAGCAACGATGCGAGGAAGCTTTAAAGCCTGTCAAAATGGTATGCAACAGTGGTCTACCGATTGCTGACAAAGCCCTCATCTACAGTCCGGATC
372 V V D Y E Q R M Q E A L K A C Q M V M Q S V Y R L L T K P S Y R L P D
381 TCAGTTTCTCGTACTTTACGCTCGACGACTCCCGCTGGCCAGGATCTGGTGGAGGACAGTGCAGAACACCATAATCTGGGCGAGGATATATGCTTCCGCTCAAGCATGT
390 F S F S Y F T L D D S R W P G S G V E D S R T T I I L G E D I L P S K H V
400 GGTGATGCACAAACCCCTGCCCACTGGCGGAGCAGCTGGTGGACTTTTATGATCCAGTCCGTTTGAAGCGTTACCGACTTGGCAAAACAACTCCGGTGGAGGCTCAG
409 V M H N T L P H W R E Q L V D F Y V S S P F V S V T D L A N N P V E A O
418 GTGTCGCGGTGGAGCTGCCACACGACACTCACAAGACTATCCACCCACAAGGCTCCACCAAGTACCGCATCTCTCAAGGCTCGGCTGCCGCCATCG
427 V S P V W S W H H D T L T K T I H P Q G S T T K Y R I I F K A R V P P M
436 GCTTGGCCACCTACGTTTAAACATCTCCGATTCCAAGCCAGAGCAGCACTCGATGATCGAATCTCTTGTCTCCGTAACAAACCCGACTTGGTACCATTTGGGCAATA
445 G L A T Y V L T I S D S K P E H T S Y A S N L L L R K N P T S L P L G Q Y
454 TCCGGAGGATGTGAAGTTTGGCGATCTCTCGAGATCTCATTGGCGGTTGGTAAACGACCCACTTGGCTTTTTCGGAGCAGGCTCTCTTAAAGTCCATTACGCTTACT
463 P E D V K F G D P R E I S L R V G N G P T L A F S E Q G L L K S I Q L T
472 CAGGATAGCCACATGTACCGGTGCATCTCAAGTTCTCAAGTATGGCGTTCCGATCCGATGGCGATAGATCCGGTGCCTATCTGTTCTCGCCCAATGGACAGCTTCCG
481 Q D S P H V P V H F K F L K Y G V R S H G D R S G A Y L F L P N G P A S
490 CAGTCGAGCTTGGCCAGCCAGTGGTCTGCTGACTAAGGCAAACTGGAGTCTGCTGAGCGTGGGACTTCCGAGCGTGGTGACACGACGATATATGCGCGGTGGTGC
500 P V E L G Q P V V L V T K G K L E S S V S V G L P S V V H Q T I M R G G A
510 ACCTGAGATTCCGAATCTGGTGGATATAGGCTCACTGGACAAACACGAGATCGTGATGCGCTTGGAGACGCATATCGACAGCGGCGATATCTTACACGGATCTCAAT
520 P E I R N L V D I G S L D N T E I V M R L E T H I D S G D I F Y T D L N
530 GGATTGCAATTTATCAAGAGGCGCGGTTTGGACAAATACCTTTGACGGCCAACTATTATCCATACCTTCTGGTATGTTCAATGAGGATGCCAATACCGCATCTACTC
540 G L Q F I K R R R L D K L P L Q A A N Y Y P I P S G M F I E D A N T R L T
550 TCTTCACGGGTCAACCGCTGGGTGGATCTTCTTGGGCTCGGGCGAGCTAGAGATTGCAAGATCGTGCCTGGCCAGCGATGAGAACCGCGCTGGGACAGGGTGT
560 L L T G Q P L G G S S L A S G E L E I M Q D R R L A S D D E R G L G Q G V
570 TTTGGACAAAGCGGCTGCTGCATATTATCGGCTGGTCTGGAGAGGTTAAACAACTGTGTCGACCGTCAAAGCTTATCTGCGGCTATTGACAAGTGGCCGA
580 L D N K P V L H I Y R L V L E K V N N C V R P S K L H P A G Y L T S A A
590 CACAAAGCATCGCAGTCACTGCTGGATCCACTGGACAAGTTTATATTCCGTGAAATGAGTGGATCGGGGACAGGGGCAATTTGGTGGCGATCATCTTCCGCTCGTG
600 H K A S Q S L L D P L D K F I F A E N E W I G A Q G Q F G G D H P S A R
610 AGGATCTCGATGTGCTGGTGGATGAGACGCTTAAACAGAGCTCGGCCAAAACCCAGCGAGTAGGCTACGTTCTGCACCGCAACAACTCATGCAATCGGCGACTCCAGA
620 E D L D V S V M R R L T K S S A K T Q R V G Y V L H R T N L M Q C G T P E
630 GGAGCATACACAGCTGGATGTGCTGCCACTACTGCCAATGTCGCGAGTGGCGAGCGCAGCGCTGACTTCTGCGCAATTTGCAAGCAATTTGGATGGCATGGTG
640 E H T Q K L D V C H L P N V A R C E R T T L T F L Q N L E H L D G M V
650 GCGCGGAAGTGTCCCATGGAAACCGCGCTTATGTGAGCAGTCACTCAAGCTGA
660 A P E V C P M E T A A Y V S S H S S
```

FIG. 29

Human mannosidase II (U31520)

```
1 ATGAAGTTAAGCCGCGAGTTCACCGTGTTCGGCAGTGGCAICTTCTGTGGTGATTCTCTGCTCTACCTGATGCTGGACGGGGTCACTTAGACTACCCAGGAACC
101 M K L S R Q F T V F G S A I F C V V I F S L Y L M L D R G H L D Y P R N
110 CGCGCCGCGAGGGCTCCTTCCCTCAGGGCCAGCTCTCAATGTTGCAAGAAAAATAGACCAATTGGAGCGTTTGGCTAGCTGAGAATAAGAGATCATCTCAAAATTATAG
37 P R R E G S F P Q G Q L S M L Q E K I D H L E R L L A E N N E I S N I R
219 AGACTCAGTCATCAATTTGAGTGAGTCTGTGGAGGATGGTCCGAAAAGTTCACAAAGCAATTTACGCCAAGGTGCTGGCTCAGATCTTCTGCCCTCACAATTATCCCTC
73 D S V I N L S E S V E D G P K S S Q S N F S Q G A G S H L L P S Q L S L
328 TCAGTTGACACTGCAGACTGTCTGTTGCTTCACAAAGTGGAAAGTCACAATTCAGATGTGCAGATGTTGGATGTTTACAGTCTAATTTCTTTGACAATCCAGATGGTG
110 S V D T A D C L F A S Q S G S H N S D V Q M L D V Y S L I S F D N P D G
437 GAGTTTGGGAAGCAAGGATTGACATTACTTATGAATCTAATGAATGGGACACTGAACCCCTTCAAGTCTTTGTGGTGGCTCATTCCCATAACGACCCAGGTTGGTTGAA
146 G V W K Q G F D I T Y E S N E W D T E P L Q V F V V P H S H N D P G W L K
546 GACTTTCAATGACTACTTTAGAGACAAGACTCAGTATATTTTAATAACATGGTCTTAAAGCTGAAAGCAAGACTCAGGAGGAAGTTTATTGGTCTGAGATCTCTTAC
182 T F N D Y F R D K T Q Y I F N N M V L K L K E D S R R K F I W S E I S Y
655 CTTTCAAAGTGGTGGATATTATAGATATTCAGAAGAAAGGATGCTGTTAAAGTTTAAATAGAAAATGGTCAGTTGAAATTTGACAGGTGGCTGGGTTATGCCTGATG
219 L S K W D I I D I Q K K D A V K S L I E N G Q L E I V T G G W V M P D
764 AAGCTACTCCACATTATTTGCCCTTAATGATCACTAATGAAGGACATCAGTGGCTGGAAAATAATATAGGAGTGAAACCTCGGTCCGGCTGGGCTATTGATCCCTT
255 E A T P H Y F A L I D Q L I E G H Q W L E N N I G V K P R S G W A I D P F
873 TGGACACTCACCACAATGGCTTATCTTAAACCGTGTGGACTTCTCATGCTTATCCAGAGAGTTCATTATGCAGTTAAAAAACACTTTGCACTGCATAAAAA
291 G H S P T M A Y L L N R A G L S H M L I Q R V H Y A V K K H F A L H K T
982 TTGGAGTTTTTTGGAGACAGAATTGGGATCTGGGATCTGTACAGATATTTTATGCCACATGATGCCCTTACAGCTATGACATCCCTCAGCTTTGGGACGTATG
328 L E F F W R Q N W D L G S V T D I L C H M M P F Y S Y D I P H T C G P D
1091 CTAATAATGCTGCCAGTTGATTTTAAACGCTTCTCTGAGGCGAGATTGGTGTGCTGGGAGTCCGCCAGAAAACAATACATCTCTGGAATGTCCAAAGCAGGGC
364 P K I C Q F D K R L P G G R F G C P W G V P P E T I H P G N V Q S R A
1200 TCGGATGCTACTAGATCAGTACCGAAGAAAGTCAAAGCTTTTTCGAACCAAGTCTCTGCTGCCCTCAGTAGGAGATGATTCCGCTACTGTGAATACACGGAATGGGAT
400 R M L L O Q Y R K K S K L F R T K V L L A P L G D D F R Y C E Y T E W D
1309 TTACAGTTTAAAGAAATATCAGCAGCTTTTGGATTATATGAATCTCAGTCCAAGTTTAAAGTAAAGATACAGTTTGGAACTTTATCAGATTTTTTGATCGCTGGGATA
437 L Q F K N Y Q O L F D Y M N S K S K F K V K I O F G T L S D F D A L D
1418 AAGCAGATGAAACTCAGAGAGACAAGGCCAATCGATGTTCCCTGTTTAAAGTGGAGATTTTTCATTATGCCGATCGAGATGATCATTACTGGAGTGGCTATTTTAC
473 K A D E T Q R D K G Q S M F P V L S G D F F T Y A D R D D H Y W S G Y F T
1527 ATCCAGACCCCTTTTACAAACGAATGGACAGAATCATGGAATCTCATTTAAGGGCTGCTGAAATTTCTTACTATTTGCGCTTGAGACAAGCTCACAATAACAGATAAAT
509 S R P F Y K R M D R I M E S H L R A A E I L Y Y F A L R Q A H K Y K I N
1636 AAATTTCTCTCATCATCTTTACACGGCACTGACAGAAGCCAGAGGAATTTGGGACTGTTTCAACATCATGATGCTATCACAGGAATGCAAAAGACTTGGGTTGGT
546 K F L S S S L Y T A L T E A R R N L G L F Q H H D A I T G T A K D W V V
1745 TGGATTATGGTACCAGACTTTTTCATTGCTTAATGGTTTGGAGAAGATAATTGGAATTTGCAATTTCTTCTTATTGGGAAGGACAAACTCAGATCAGCTTACTC
582 V D Y G T R L F H S L V L E K I I G N S A F L L I G K D K L T Y D S Y S
1854 TCCTGATACCTTCTCGGAGATGGATTGAAACAAAATCACAAGATTTCTCGCCACAAAAAATAATAAAGGCTGAGTGGGAGCCAGGTAACCTTGTGGTCTATAAT
618 P D T F L E M D L K Q K S Q D S L P Q K N I I R L S A E P R Y L V Y N
1963 CTTTGAACAAGACCGAATCTCGTTGGTCTCAGTCTATGTAGTTCCTCCGACATGCAAGTGTCTCTGCTTCAGGAAAACCTGTGGAAGTTCAAGTCAGCGCAGTTT
655 P L E Q D R I S L V S V Y V S S P T V Q V F S A S G K P V E V Q V S A V
2072 GGGATACAGCAAAATACTATTTCAGAAACAGCCTATGAGATCTCTTTTCAGACATATACCGCCATTGGGACTGAAAGTGATAAGATTTTGGAATCAGCAAGTTCAA
691 W D T A N T I S E T A Y E I S F R A H I P P L G L K V Y K I L E S A S S N
2181 TTCACATTTAGCTGATTATGTCTTGATAAGAATAAAGTAGAAGATAGCGGAATTTTACCATAAAGAAATATGATAAATCTGGAAGAGGTATAACACTAGAGAACTCC
727 S H L A D Y V L Y K N K V E D S G I F T I K N M I N T E E G I T L E N S
2290 TTTGTTTTACTTCGGTTTGTATCAAACTGGACTTGAAGCAATGATGACTAAGGAAGATGGTAAACACCATGAAGTAAATGTGAATTTTCATGGTATGGAACCAAA
764 F V L L R F D O T G L M K Q M M T K E D G K H H E V N V Q F S W Y G T T
2399 TTAAGAGACAAAAGTGGTGCCTACCTCTTCTTACCTGATGGTAATGCCAAGCCTTATGTTTACACAACACCGCCCTTGTGACAGTGACACATGGAAGGATTTATTC
800 I K R D K S G A Y L L F L P D G N A K P Y V Y T T P P F V R V T H G R I Y S
2508 GGAAGTGACTGCTTTTTGACCATGTTACTCATAGAGTCCGACTATACACATACAGGGAATAGAAAGCAGTCTGTGGAAGTTTCCAATATGTGGACATCCGAAAA
836 E V T C F F D H V T H R V R L Y H I Q G I E G Q S V E V S N I V D I R K
2617 GTATATAACCGTGAGATTGCAATGAAAAATTTCTCTGATATAAAAGCCAAAATAGATTTTATACTGACCTAAATGGGTACCAGATTCAACCTAGAATGACACTGAGCA
873 V Y N R E I A M K I S S D I K S Q N R F Y T D L N G Y Q I Q P R M T L S
2726 AATTGCCCTTCAAGCAAAATGCTATCCCATGACCACAATGGCCTATATCCAGGATGCCAAACATCGTTTGACACTGCTCTGCTGCTCAGTCATTAGGGGTTTCAGTTT
909 K L P L Q A N V Y P M T T M A Y I Q D A K H R L T L L S A Q S L G V S S L
2835 GAATAGTGGTCAGATTGAAGTTATCATGGATCGAAGACTCATGAAGATGATAATCGTGGCCTTGAGCAAGGTATCCAGGATAACAGATTACAGCTAATCTATTTTGA
945 N S G Q I E V I M D R R L M Q D D N R G L E Q G I Q D N K I T A N L F R
2944 ATACTACTAGAAAAAGAGTGCTGTTAATACGGAAGAGAAAGAGTGGTCAAGTATCCTTCTCTCTTACGCCACATAACTTCTTCTCATGAATCACTCAGTCA
982 I L L E K R S A V N T E E E K K S V S Y P S L L S H I T S L M N H P V
3053 TTCCAATGGCAAAATAGTTCTCTCCTCAGTACCTTGAAGTGGCAAGTGAATTTCTCCATTACAGTCACTTTTGCCTTGTGACATTCATCTGGTTAATTTGAGAAACAT
1018 I P M A N K F S S P T L E L Q G E F S P L Q S S L P C D I H L V N L R T I
3162 ACAGTCAAAGGTGGGCAATGGGCACTCCAATGAGGAGCCTTGATCCTCCACAGAAAAGGGTTTGATTGTGCGTTCTCTAGCAAAGGCAAGGCTGTTTGTCTACT
1054 Q S K V G N G H S N E A A L I L H R K G F D C R F S S K G T G L F C S T
3271 ACTCAGGGAAGATATTGCTACAGAACTTTTAAACAAGTTTATTGTCGAAAGTCTCACACCTTCATCACTATCCTTGATGCATTACCTCCCGGCACTCAGAAATATA
1091 T Q G K I L V Q K L L N K F I V E S L T P S S L S L M H S P P G T Q N I
3380 GTGAGATCAACTGAGTCCAATGGAATCAGCACATTCGAATCCAGTTGAGGTGA
1127 S E I N L S P M E I S T F R I Q L R
```

FIG. 30

Mouse mannosidase II (X61172)

```
1 ATGAAGTTAAGTCGCCAGTTACCGTGTGGCAGCGCATCTCTCGTCTGAATCTTCTCACTCTACCTGATGCTGGACAGGGGTCCTTGGACTACCCCTCGGGGCC
111 M K L S R Q F T V F G S A I F C V V I F S L Y L M L D R G H L D Y P R G P
112 GCOCAGGAGGGCTCTTCCGAGGCCAGCTTTCAATATGCAAGAAAGATTGACCATTTGGAGCGTTTGTCTGCTGAGAACAACGAGATCATCTCAATATCAGAG
377 R O E G S F P Q G Q L S I L Q E K I D H L E R L L A E N N E I I S N I R
221 ACTCAGTCATCAACCTGAGCGAGTCTGTGGAGGACGGCCCGGGGGTCCAGGCAACGCCAGCCAGGCTCCATCCACCTCCACTCGCCACAGTTGGCCCTGCAGGCT
74 D S V I N L S E S V E D G P R G S P G N A S Q G S I H L H S P Q L A L Q A
331 GACCCAGAGACTGTTTGTGCTTACAGAGTGGGAGTCAGCCCGGGATGTGCAGATGTTGGATGTTTACGATCTGATTCCTTTTGATAATCCAGATGGTGGAGTTG
111 D P R D C L F A S Q S G S Q P R D V Q M L D V Y D L I P F D N P D G G V W
441 GAAGCAAGGATTTGACATTAAGTATGAAGCGGATGAGTGGACCATGAGCCCTGCAAGTGTGTGTGGTGCCTCACTCCCAATGACCCAGGTTGGTTGAAGACTTCA
147 K O G F D I K Y E A D E W D H E P L Q V F V V P H S H N D P G W L K T F
551 ATGACTACTTTAGAGACAAGACTCAGTATATTTTAAATACATGGTCTAAAGCTGAAAGAAAGACTCAAGCAGGAAGTTATGTGCTCTCAGATCTCTTACCTTGCAAAA
184 N D Y F R D K T Q Y I F N N M V L K L K E D S S R K F M W S E I S Y L A K
661 TGGTGGGATATTATAGATTTCCGAAGAAGGAGCTGTTAAAGTTTACTACAGAATGGTCAGCTGGAATTTGTGACCGGTGGCTGGGTTATGCCTGATGAAGCCACTCC
221 W D I I D I P K K E A V K S L L Q N G Q L E I V T G G W V M P D E A T P
771 ACATTATTTTCCCTTAATTGACCACTAATTGAAGGGCACCATGGCTGGAAGAAATCTAGGAGTGAAACCTCGATCGGGCTGGGCTATAGATCCCTTTGGTCAATTCAC
257 H Y F A L I D Q L I E G H Q W L E K N L G V K P R S G W A I D P F G H S
881 CCACAATGGCTTATCTTAAAGCGTGTCTGGATTTTACACATGCTCTCAGAGAGTCCATTATGCAATCAAAAAACACTTCTCTTGGCAAAAACGCTGGAGTTTTC
294 P T M A Y L L K R A G F S H M L I Q R V H Y A I K K H F S L H K T L E F F
991 TGGAGACAGAATTGGGATCTTGGATCTGCTACAGACATTTGTGCCATATGATGCCCTTCTACAGCTACGACATCCCTCACACCTGTGGGCTGATCTAAATATCTG
331 W R O N W D L G S A T D I L C H M M P F Y S Y D I P H T C G P D P K I C C
1101 CCAGTTGATTTTAAACGGCTTCTCGAGGCGAGATATGGTGTCCCTGGGGAGTTCGCCAGAACCAATCTCCTGAAATGTCCAAAGCAGGGCTCAGATGCTATGG
367 O F D F K R L P G G R Y G C P W G V P P E A I S P G N V Q S R A Q M L L
1211 ATCAGTACCGGAAAAAGTCAAACTTTTCCGCACTAAAGTTCTGCTGGCTCCACTGGGAGACGACTTTCGGTTCACTGAATACACAGAGTGGGATCTGCACTGCAGGAAC
404 D Q Y R K K S K L F R T K V L L A P L G D D F R F S E Y T E W D L Q C R N
1321 TACGACCACTGTTTCACTTACATGAAGTCCGAGCTCATCTGAAAGTGAAGATCCAGTTTGGAACTTGTGAGATATTTCGACGATTTGGAGAAAGCGGTGGCAGCGCA
441 Y E Q L F S Y M N S Q P H L K V K I Q F G T L S D Y F D A L E K A V A E
1431 GAAGAAGACTAGCCAGTCTGTGTTCCCTGCCCTGAGTGGAGACTTCTTCACTAGCTGACAGAGACGACCATTAAGTGGAGTGGTCTACTCAGCTCCAGCTTTCTACA
477 K K S S Q S V F P A L S G D F F T Y A D R D D H Y W S G Y F T S R P F Y
1541 AACGAATGGACGAATAATGAATCTGCTATAAGGGCTGCTGAAATCTTTTACAGTTTGGCTTGAAGAACAGCTCAGAAATACAAGATAAAATTTCTTTCATCACT
514 K R M D R I M E S R I R A A E I L Y O L A L K Q A Q K Y K I N K F L S S P
1651 CATTACACACACTGACAGAAGCGAGGAAGTCTAGGACTATTTAGCATATGATGCCCTTCTACAGCTACGACATCCCTCACACCTGTGGGCTGATCTAAATATCTG
551 H Y T T L T E A R R N L G L F Q H H D A I T G T A K D W V V V D Y G T R L
1761 CTTTCACTTAAATCTTTGGAGAAGATAATGGAGATTTCTGCTTCTTCTCATTTTAAAGCAAAAAAGCTGACAGTCCATCTTCCAAAGCTTCTTAGAGA
587 F Q S L N S L E K I I G D S A F L I L K D K K L Y Q S D P S K A F L E
1871 TGGATACGAAGCAAGTTTCAAGATTTCTTCCCAAAAAATTTAATACAACTGAGCGCACAGGAGCAAGGTACTTGTGGTCTACAATCCCTTTGAACAAGAACGG
624 M D T K Q S S Q D S L P Q K I I I Q L S A Q E P R Y L V Y N P F E Q I R
1981 CATTGAGTGTGCTTCCAGTCCGGTAACTCCGCCACAGGGAAGTGTGTCTGATTGCGGAAAAACCGGTGGAGGTTCAAGTCACTGCAATTTGCAACGACATGAGGACAAT
661 H S V S I R V N S A T G K V L S D S G K P V E V Q V S A V W N D M R T I
2091 TTCACAAGCAGCTATGAGGTTTCTTTTCTAGCTCATATACCACCTGGGACTGAAAGTGTTAAGATCTTAGAGTCAACAAGTCAAGCTCACACTTGGCTGATTATG
697 S Q A A Y E V S F L A H I P P L G L K V F K I L E S Q S S S S H L A D Y
2201 TCCTATATAAATGATGGACTAGCAGAAATGCAATATTCCAGTGGAAGAACATGGTGGATGCTGGAGATGCCATAACAATAGAGAAATCCCTTCTGGCGGATTTGGGTTT
734 V L Y N N D G L A E N G I F H V K N M V D A G D A I T I E N P F L A I W F
2311 GACCGATCTGGCTGATGGAGAAAGTGAAGAAGAAAGACAGTACAGAGTGAAGTGAAGTCCAGTTCTGTGGTACGGAACCAACAAAAAGGACAAAGACGG
771 D R S G L M E K V R R K E D S R Q H E L K V Q F L W Y G T T N K R D K S G
2421 TGCTACCTCTCTCTGCTGACGGGCGAGGCCAGCCATATGTTTCCCTAAGACCGCCCTTGTGAGAGTGACAGCTGGAAGGATCTACTCAGATGTGACCTGTTCTCTG
807 A Y L F L P D G Q G Q P Y V S L R P P F V R V T R G R I Y S D V T C F L
2531 AACACGTTACTCACAAGTCCGCTGTACAACATTCAGGGAATAGAAGTCACTGCTCAATGGAAGTTTCTAATATTGTAACATCAGGAATGTGCAATACCGTGAGATTGTA
844 E H V T H K V R L Y N I Q G I E G Q S M E V S N I V N I R N V H N R E I V
2641 ATGAGAATTTCTATAAATAAACCAACCAATATGATATTAAGTCACTAATGGATATCAGATTGAGCTTAGAAGGACCATGAGCAAAATGGCTCTTCAAGCCAACGT
881 M R I S S K I N N Q N R Y T D L N G Y Q I Q P R R T M S K L P L Q A N V
2751 TTACCCGATGTGCAATGGCTATATCCAGGATGCTGAGCACCGGCTCAGCTGCTCTCTGCTCAGTCTCTAGGTGCTTCCAGATGGCTTCTGGTCAGATTGAAGTCT
917 Y P M C T M A Y I O D A E H R L T L L S A Q S L G A S S M A S G Q I E V
2861 TCATGGATCGAAGGCTCATGAGGATGATAACCGTGGCTTGGGCAAGGCTCCATGACAATAAGATTACAGCTAATTTGTTTGAATCCCTCTCGAAGAGAGAACGGCT
954 F M D R R L M Q D D N R G L G Q G V H D N K I T A N L F R I L L E K R S A
2971 GTGAACATGGAAGAAGAAAGAGAGCCCTGTGAGTACCCTTCCCTCTCAGCCATGACTTCTGCTTCTCAACCATCCCTTTCTCCCATGGTACTAAGTGGCCA
991 V N M E E E K K S P V S Y P S L L S H M T S S F L N H P F L P M V L S G Q
3081 GCTCCCTCCCTGCTTGTAGCTGCTGAGTGAATTTCTCTGCTGCTGCTCTCTACCTTGTGATATCCATCTGGTCAACCTCGGCAACATAACAAGATGGGCA
1027 L P S P A F E L L S E F P L L Q S L L P C D I H L V N L R I Q S K M G
3191 AAGGCTATTGCGATGAGGAGCCTTGTATCTCCACAGGAAGGCTTGTGATGCGAGTTCTCCAGCAGAGGACATCGGGCTACCTGTTCCACTACTCAGGGAAGATGTCA
1064 K G Y S D E A A L I L H R K G F D C Q F S S R G I G L P C S T T Q G K M S
3301 GTTCTGAACTTTTCAACAAGTTTCTGTGGAGAGTCTGCTCCCTTCTCTGCTGCTGATGCACTCCCTCCAGATGCCAGAACATGAGTGAAGTCAAGCTGAGCCC
1101 V L K L F N K F A V E S L V P S S L S L M H S P P D A Q N M S E V S L S P
3411 CATGGAGATCAGCAGTTCCGTATCCGTTCGGTTGGAGCTGA
1137 M E I S T F R I R L R W T
```

Rat mannosidase II (XM 218816)

1 ATGGCGCTGTATAGCGTGAGCGCCAGGGGCAACGGCAGGCGGTGGAAAAAGAACTCTCCACCAAGGGTATCCGTGGAAAGCCAATGACCAATGGCAGCTGCTCAGAACTG  
109 GCATTGCTCAGCAAAAAGGAGGTACTGTACACAGGAGTGTGTGAGCGCCACAGGAGTACAGCTGAAAAAAGTCTCAAGACCAACATGATATCAGAGTGTGCTGCTGT  
37 ALLSKTRMYCHQGCVRPRTDVKNKFTTDTTDTQSVVP  
217 GTGCAATTGAAGCTGAAAAAGCAGGTGACAGTGTGCGGGGCTGCTATCTTGTGTGGCGCTCTTCCCTGTACCTAATGCTGGACGAGTGAGCATGATCTCGCC  
73 VSMKCLKKQVTVCGA AIFCVAVFSLYLMLDRAVRQHDPA  
325 AGACACAGCAATGGTGGGAATCTCCCGAGGACCAATTTCTGTCTACAGAACCGGATCGAACAGCTGGAACAGCTGCTGGAAGAAAACCATGAGATCAAGCCAT  
109 RHQNGNGNFRPSQISVLQNRIEQLEQLLENHEIISH  
433 ATCAAGCACTCTGTGTCGAACGTGACAGCCAATGCGAGGGGCCACAGCCCTGTCTGCCCTACCAACAGCAGCAAGCGCTCTGGGCTGTGCTCCCGGAGCCCGGGCC  
145 IKDSVLELTANAEGPPALLPYHTANGSWAVLPEPRP  
541 AGCTCTCTCTGTATCCCTGAGGAGTCCGAGTTGTCTTGGGGGCGGGGTGAGAAGCAGAGCTACAGATCTTAACGTGTCTGAGGAGTTGCCGTTTGACAT  
181 SFFSVSPEDCFALGGRGKPELQMLTVSEDLFDN  
649 GTGAGGGGCGGCTGTGGAGGCAAGGCTTCGACATCTCTACAGCCCAATGACTGGGATGTGAAGACTGCAGGTGTTTGTGGTGGCTCACTCCCAATGATC  
217 VEGGVWRQGFDSISYNDWDADLELQV FVVP HSHNDP  
757 GGTGAAGAGCAGCAGGCCAGGCTGAGGTCGAGGTTGGGCTTCTGTGGACAGGCTGTGATCAAGACTTQVACAAGTACACAGGAACAAACCAACATCT  
253 GE E P A G P S R S V Q G G L G D R R W I C T F D K L Q Y T E O T Q H I  
865 CTCACAGCATGGTGTCCAAGTGTGAGGAAGATCCCCGAGGCGCTTCTCTGGGCAGAAGTCTCTCTTCCGCAAGTGGTGGGACCAACATCAGTGGCCCAAGAG  
289 LNSMVSKLQEDPRRRFLWAEVSFFAKWWDNISAQKR  
973 GCAGCAGTCTGAAGAGTGGTGGGAATGGGACAGTGGAAATGCAACGGGTGATGGGTGATGAGCAGATGAGGCAACTCCCAATCTTCCCTCTGGTGGGGCAGCTC  
325 AAVRRLV L N G N Q L E I A T G G W V M P D E A N S H Y F A L V G Q L  
1081 ATCAGAGGGGCCCCCGGTACGACAGGCGAGTGGACCCCTTGGACAGCAGCTCCACATGCTTACCTGCTGCGCGCTGCCAACCTGACAGCAGTGCATTAATCAGAG  
361 IEGPPVVRRAVDPFHGSSTMPYLLRANLTSMLIQ  
1189 GTGCATTAGCCCATCAAGAAGCACTTTCGGGCCATCAGACCTGGAGTTCATGTGGAAGCAGACATGGGATTTCAGACTTCAGCAGCAGACATCTTTCGCCACATGATG  
397 VHYAIAKHHFAATHSLFEMWRTQWDS DSTDIFCHMM  
1297 CCCCTCTACAGTACGACGCTCCCAACACCTGTGGCCCTGATCCCAAGTGTGTCGCGAGTTGATTCAAAGCTGCGCGGTGGGAGAACTCAATGTCTCTGGAAG  
433 PFFYSYDVPHTCGGCGDPDKICCGQDFDKRLPGGTRINCPWK  
1405 GTGCGCGCGGGCTATCAGCAGGCAACAGTGGCGAGCGCCCTGCTCTGGACAGTACCGGAAGAAGTCCCGGCTGTTTGAAGCAGTGTCTCTCTGTG  
469 VPPRAITEANVADRAALLDQYRKKSRLFRSSVLLV  
1513 CCGCTGGGTGATGATCTCCGATGACAAGCCAGGAATGGGATGCCAGTCTTCAACTATCAACGGCTCTTTCGATCTCCCAACAGCAAGCCGAGGTTCACAGTA  
505 PLGDDFRYDKPEQWDAQFFNYQR LFDLNSKPEFHV  
1621 CAGGCAAGTGTGGGCACTCTCTGATATTGTATGCCCTGTATAAGAGGACAGGAGTGAGGCTGGTGCGCGGCTCCAGGTTCTCTGTCTGAGTGGGAGCTC  
541 QAQFGTLESEYFDALYKRTGVEPGARP GPFPVLSGD  
1729 TTTCTCTATGTGACCGGGAGGACCACTACTGGACAGGCTATTACACTTCCCGGCTTCTATAAGAGCTTGGACCGGCTGTAGAACTCACTTCTGTGGGCGAG  
577 FTSYADREDHYWTGYYSRPFYKSLDRVLRLGAE  
1837 GTCTATACAGCTGGCTTGGCGGCTGCGCCGCTGTGGACTGATGGCAGTACCGCTGTGATTACGCTGTGCTGACGGAAGCTGCTGTACATGGGCGCTC  
613 VLYSLALAHARRSGLTGQYPLSDYAVLTL EARTLRGL  
1945 TTCAGCACAGATGCCATCAGGAACGTGCAAGGAGGAGTGTAGTAGACTATGGGCTCAGGTTGCGGTTCCCTGGTCAGGCTTAAGCAGGATCATCAAT  
649 FQHDAITGTAKAEAVVDYGVRLRLSLVSLKQVIIN  
2053 GTGCGCACTACTGGTGTGGGGGCAAGGAGCACTACAGCTTTGACCTTAGGCAACCCTTCTCTCAAATGGTGAGCCAGGCTGGCGAGGCTCTCAGAGCAACCTC  
685 AAHYLV L G D K E T Y S F D P R A P F L Q M V S Q A W R G S Q S T L  
2161 CAGCCAGCGCGGGCTTGTCTGCTGTGCTCTGCGCTGCGCGAGGAGCTCTAGGTTTGTGGTGTCTTAAACCACGTGAACAGGAGCGGCTCAGT  
721 HPSAALVPA A A A S A L L Q R A P R F V V F N P L E Q E R L S  
2269 GTGGTGTCTGCTGGTCAACTACCCCGAGTGGAGTGCTTTCAGAGGAGGGTCAGCCCTGTCTGTGCGAGATCAGTGTGAGTGGAGCTGCCCAACACATGGT  
757 VVSLVNSPRVRLVLS E E G Q P L S V Q W S S A T N M V  
2377 CCGGATGTCTACAGGTTGTCAGTGCCTTCTGCGCTGCGAGCCCTGGGCTGGGTGTGCTGAGCTGCAAGCAGATCTCGATGGACCTACACATGCACTGCTTCCGGT  
793 PDVYQVSVVPVRLPALGLGLVLQLQPLDGPYTLQSSV  
2485 CATGCTTACCTGAACCGGCTGAACTGTCTGACAGGCAACAACTTCTCTGCTGTGTGGAATCGGGACAGGATGCTCGCCATCAGCAATCGATCATG  
829 HVYV L N G V K L S V S R Q T T F P L R V V D T S G T S D F A I S N R Y M  
2593 CAGGTTCTGGTCTCCGCGCTTACTGGGCTTCAAGAGCTCCGACGTGTGGACGAAGAGCAGGACAGCAGGTGGACATGAAGCTCTTCTGTATGGAACCCGACA  
865 QVWFSG L T G L L K S V R R V D E E Q E Q V D M K L F V Y G T R T  
2701 TCCAAGGATAAGAGTGGTGCTACTCTCTCTGCTGATAACGAGGCTAAGCCCTATGCTCTCAAGAAACCTCTGTGCTGCGCGTCAACGAAGGCCCTTCTCTCA  
901 SKDKS G A Y L F L P D N E A K P Y V P K K P P V L R V T E G P F S  
2809 GAGGTGGCTGCGTATTATGAGCACTTACCAAGTATTGCACTTTACAACCTGCGAGGGGTAGAGAGGCTGTCTCTGGAGTGTGCTTCAAGTGAGCATCAGGGA  
937 EVAAYEHFHQVIRLYNLPGVEGLSLDVSVFQVDIR  
2917 TACGTGAACAGGAGCTAGCCCTCGCATCTCACACAGATCGACGCGAGGCGACTTTTTCACAGACTCAATGGCTTTCAGGTACAGCCCGGAGATATCTGAAG  
973 YVNXELALRIHTDIDSQGTFFD L N G F O V Q P R K Y L K  
3025 AAGTGGCCCTCAGGCTAATTTTACCCTATGTCAGGTATGCTCATCTCAGGATTCGAGGAGGCGCTCAGCTGCACATGCTCAGGCTCTGGGTTCTCCGAG  
1009 KLP L Q A N F Y P M P V M A Y I Q D S Q R R L T L H A Q A L G V S S  
3133 CTCGGCAATGCCAGCTGGAGGTATCTGGACCGAAGGCTAATGCAAGATGACAACCGGGACATAGGCCAAGGGCTCAAGACAACAGATCACTTGCACCAATTC  
1045 L G N G Q L E V I L D R R L M Q D D N R G L G Q G L K D N K I T C N H F  
3241 CGGCTCTGTAGAAAGCTGGAACCTGATGAGGCTCGAGGTCAACAGAGGCTCTTACAAGCTACCGCTCCCTCTCAGGCACATGACTCCATCTGACTTCAACACA  
1081 R L L L E R T L M S P E V Q Q E R S T S Y P S L S H M T S M Y L N T  
3349 CTTCTCTGGTCTTACCGGTGGCAAGGAGGAGACAGCAGCCCACTCTGCACTTTTACCCTCTGCTCTCTCGTGTGCCCTGGCATTTCACTGCTCAATCTG  
1117 P L V L P V A K R E S T S P T L H S F H P L A S P L P C D F H L L N  
3457 CGCATGCTCCCCCGAGGTGAGTGTCCCGGTCCGTGCCAATCTCAACATCAGGCTGAGGCTTGCCTTCTGGCAGACATGCTGCTGACCTCCACCGCTCTTGTG  
1153 R M L P A E V S V P V R A N P H Q A E G G T T L L G R H A D P P P L L S  
3565 CTGACGTCTTCAGGACCACTTGGCCGGGCTGATGCTGCTCTCATCTCAACGCAAGGPTTGTAGCTGGGCTGTGAAGCCAAAGACCTGGGCTTCACTGTACC  
1189 L T V F Q D T L P A A D A A L I L H R K G F D C G L E A K N L G F N C T  
3673 ACAAGCAAGGCAAGCTGGCCCTGGGAGCCTTCCATGGCCGTGATGTGATTCTCGAGCCAGCCCTTTTGACTTGTATACCTCTGGGCTCGGCTCCCAAC  
1225 T S Q G K L A G S L F H G L D V L L Q P T S L T L Y P L A S P S N  
3781 AGCACTGACATCTCTGAGGCGCATGGAGATCAGCACTTCCGCGCTGCGCTTGGGTTAG  
1261 S T D I S L E P M E I S T F R L R L G

FIG. 32

Human mannosidase IIx (D55649)

```
1 ATGAAGCTGAAAGACAGGTGACACTGTGTGGGGTCCCATCTTCTGTGTGGCAGTCTTCTCGCTCTACCTCATGCTGGACCGAGTGCAACACGATCCACCCGACACC
101 MKLKKKQVTVCGAAIFCVAVFSLYLM LDRVQH DPTRH
110 AGAATGGTGGGAACTTCCCGGAGCCAAATTTCTGTGCTGCAGAACCCGATCTGAGCAGCTGGAGCAGCTTTGGAGGAGAACCATGAGATTACAGCCATATCAAGGA
37 QNGGNFPRSQISVLQNRIEQLEQLLEENHEIISHIKD
219 CTCCGTGCTGGAGCTGACAGCCAACGAGGAGGCGCGCCGCTGCTGCTCTACTACAGGTCAATGGCTCTGGTGGTGGCCACCGGAGCGCGCCGCGCTTCTTC
73 SVLELTANAEGPPAMLPYYTVNGSWVVPPEPRPSFF
328 TCCATCTCCCGCAGGACTGCCAGTTTGTCTTGGGGGGCGGGGTGAGAGCCAGAGCTGCAGATGCTCACTGTGCGGAGGAGCTCCGCTTTGACACGTGGATGGTG
110 SISPQDCQFALGGRGQKPELQMLTVSEELPFDNV DG
437 GTGTCTGGAGGCAAGGCTTCACATCTCTACGACCCGACGACTGGGATGCTGAAGACCTGCAGGTGTTGTGGTGGCCCACTCTCAATGACCCAGGCTGCATCAA
146 GVVWRQGFDISYD PHDWAEDLOV FVVP HSHNDPGWIX
546 GACCTTTGACAAGTACTACACAGCAGACCCCAACCATCTCTAATGCTGCTAAGCTGAGGAGGACCCCGCGCGCTTCTCTGGGACAGAGGTCTCTCTTC
182 TFDKYYTEQTQHILNSMVSKLQEDPRRRFLWAEVSF
655 TTCGCAAGTGGTGGGACCAATCAATGTCCAAAGAGAGCGGCACTCCGAGGCTGGTGGGAAACGGGACGCTGGAGATTGCGACAGGAGGCTGGTGATGCCAGATG
219 FAKWWDNIN VQKRAAVRRLVGNGL EIA TGGWVMPD
764 AGGCCAATCCCACTACTTTGATTGATGACGAGCTCATCGAAGGACACGAGTGGCTGGAGAGAAATCTGGTGAACCCCGCTCTGGTGGGAGGCTGGGACCCCTT
255 EANSYFALIDQLIEGHQWLERNLGATPRSGWAVDPF
873 TGGATACAGCTCCACCATGCTTACCTGCTGCGCGCTGCCAAGCTCACCAGCATGCTGATTGAGAGAGTGCATATGCCATCAAGAAGCACTTTGCTGCCACCCACAGC
291 GYSSTMPYLLRRANLTSMLIQRVHYA IKKHFAATHS
982 CTAGAGTTCATGTGGAGGACAGACATGGGACTCGGACTCCAGCAGACAGATCTTGTGCATGATGCCCTTCTACAGCTATGAGTCCCCCATCTGTGGCCAGATC
328 LEFMWRQTWDS DSSDIFCHMMMPFYSYDVPH TCGPD
1091 CCAAGATCTGCTGCCAATTTGATTTCAAACGCTGCTGCTGGGCGCATCAACTGCTTGGAGCTGCCACCCGCGGCTCTGAGGAGGCAAGCTGGCAGAGAGGGC
364 PKICCCQFDFKRLPGGRINCPWKVP PRAITEANVAERA
1200 AGCCCTGCTTCTGGACCAATACCGAAGTCCGAGCTGTTCGGAAGCAAGCTCTCTGCTGCTTCTGGAGATGACTTCCGATATGACAAGCCCGAGGAGTGGGAT
400 ALLLDQYRKKS QLF RSNVLLVPLGDD FRYDKQEW
1309 GCCCAGTTCTCACTACCAAGGCTCTTTGACTTCTCAACAGCAGGCTTAACCTCATGTGAGGCCAGTTTGGCACTCTTCTGACTATTTGATGCCCTGTACA
437 AQFFNYQRLDFDFNSRPNLHVQA QFGTLSDYFDALY
1418 AGAGGACAGGGGTGGAGCCAGGGCGCGCTCCAGGCTTCTGCTGAGCGGGGATTCTCTCTATGCGGACCGGGAGGATCAITTCGACAGGCTATTACAC
473 KRTGVEPGARPPGFPLVSGDFFFSYADREDHYW TGYTYT
1527 TTCGCGCCCTCTACAGAGCTTAGACCGAGCTCTGGAAGCCACCTCGCGGGGCGAGAGTCTGTACAGCTGGCTGACGCTCAGCTCGCGCTGTCTGGCT
509 SRPFYKSLDRVLEAHLRGAEVLYSLAAAHARRSGLA
1636 GGCGGCTACCCATGCTGATTACCTCCCTGACGGAAGCTCGGCGGACATCTGGGGCTCTCCAGCATCAGATGCCATCACTGGCAGGCGCAAGGAGGCTGTGGTGG
546 GRYPLSDFTLLLEAARRTLGLLFQH HDAITGTAKAEAVV
1745 TGGACTATGGGGTCAAGCTTCTGCGCTCTCTGCAACCTGAAGCAGGTCATCTATGCAAGCCCACTATCTGGTGTGGGGGACAGGAGACCTACCACTTTGACCC
582 VDYGVRLRLSLVNLKQV IHA AHYLV LVLGDKET YHFD P
1854 TGAGCGCCCTCTCTCAAGTGATGACTCGCTTAAGTACGACGCGCTCCGAGCGGACCGGTGATCCAGCTGGATTCTCGCCAGGTTTGTGGTCTTATCAAC
618 EAPFLQVDOTRLSDHDA LERTV IQLDSSFRVLFN
1963 CCAGTGAACAGGAGGATTCAGCATGCTGCTGCTGCTCAACTCTCCCGCGTGGTGTCTTTCGGAGGAGGGTCAAGCCCTGGCGTGCAGATCAGGCGACACT
655 PLEERFSMLVNSPRVRVLS EEGQPLAVQISAH
2072 GGAGCTCTGCCACGAGGCGGCTCTGACGTCTACAGGTGCTGTGCTGCTGCGCTGCCAGCCCTGGGCTGGGCTGTGAGCTACAGCTGGGCTGGATGGCA
691 WSSATEAVPDVYQVSV PVRPLPALGLGLV LQLGLDGH
2181 CCGCAGCTGCGCTCTCTGTGCGCATCTACCTGCACGCGCGGCGAGTCTCCGTGACGAGGACGAGCGTTCCTCTCCGTGTCTGACTCTGGCAGCAGGACTTC
727 R T L P S S V R I Y L H G R Q L S V S R H E A F P L R V I D S G T S D F
2290 GCCCTCAGCAACCGTACATGCAAGTCTGGTCTCAGGCTTACTGGGCTCTCAAGAGCATCCGAAGGGTGGATGAGGAGCAGGACGAGGCTGGACATGCAAGTCC
764 A L S N R Y M Q V W F S G L T G L L K S I R R V D E E H E Q Q V D M Q V
2399 TTGTCTATGGCACCCGTACGTCCAAAGACAAGAGTGGAGCTACTCTTCTGCTGCGATGGCGAGGCTAGCCCTACGTCCTCCAAAGGAGCCCGCTGCTGCTGCTACT
800 L V Y G T R T S K D K S G A Y L F L P D G E A S P T S P R S P P C C V S L
2508 GAAGGCCCTTTCTCTCAGAGTGGTGGTACTATGACACATTCACAGGCGGTCGCGCTTACAATCTGCCAGGGGTGGAGGGGCTGTCTCTGGACATATCATCC
836 K A L S S Q R W L R T M S T F T R R S G F T I C O G W R G L W T Y H P
2617 TGGTGGACATCCGGGACTACGTCAACAAGGAGTGGCGCTGCACATCCATACAGACATCGACAGCCAGGCTGCAGCCCGAGCGTATCTGAAGAAGTCCCCCTCCAGG
873 W W T S G T T S T R S W P C T S I Q T S T A R V Q P R R Y L K K L P L Q
2726 CCAACTCTACCCATGCCAGTCAATGCTATATCCAGGACGACAGAAGCGCTCAGCTGCACACTGCCAGGCGCTGGGTGTCTTAGCTCAAGATGGCCAGCT
909 A N F Y P M P V M A Y I Q D A Q K R L T L H T A Q A L G V S S L K D G Q L
2835 GGAGGTGATCTGGACCGGCGCTGATGAGGATGACAACCGGGCTAGGCCAAGGGCTCAAGGACAACAAGAGAACTGCAACCGTTTCCGCTCTGCTAGAGCGG
945 E V I L D R L M Q D D N R G L G Q G L K D N K R T C N R F R L L L E R
2944 CGAACCGTGGGCACTGAGGTCCAAGATAGCCACTTACAGCTACCCATCCCTCTCAGCCACCTGACCTCCATGTACCTGAACCGCCCGGCTGCTGCTGCTAG
982 R T V G S E V Q D S H S T S Y P S L L S H L T S M Y L N A P A L A L P V
3053 CCAGGATGCAAGCTCCAGGCGCTGCTGCTGCTCATTTCTCTGCTTCTCTCACTGCGCTGTGACTTCCAGCTGCTCAACTACGTCAGCTCCAGGCTGAGGAGGA
1018 A R M Q L P G P G L R S F H P L A S S L P C D F H L L N L R T L Q A E E D
3162 CACCTACCTCGCGGAGACCGCACTCTTACACCGCAAGGTTTGTACTGCGCTGGAGGCCAAGAACTTGGGCTTCACTGCACCAAGCAAGCAAGGTA
1054 T L P S A E T A L I L H R K G F D C G L E A K N L G F N C T T S Q G K V
3271 GCCTGGGCGAGCTTTTCCATGGCTGGATGGTATTCTTCAAGCAACCTCTTACGCTTACTGTACCTCTGGCTCCCGCTCCCAACAGCACTGAGCTCTATTGG
1091 A L G S L F H G L D V F L O P T S L T L L Y P L A S P S N S T D V Y L
3380 AGCCCATGGAGATGCTACTTTTCGCTCCGCTGGGTAG
1127 E P M E I A T F R L R L G
```

FIG. 33

Insect cell mannosidase III (AF005034)

```
1 ATGAGGAGCTCGTGTCTTCTGTTGCGGCGCTTCTCCACCGGATCCTGCTGCTGCTATTGTCCTTGGGTTTGGGGTCTACTGCTATTCTACAATGCATCTCTCTCA
111 M R T R V L R C R P F S T R I L L L L L F V L A F G V Y C Y F Y N A S P Q
112 GAACATATAACAAACCAAGATCAGTTACCCAGCGAGTATGGAGCACTTCAATCTTCCCTCACTCACACCGTCAAGAGCGGAGCGGCAACTCCGGATCAATGCCCTG
377 N Y N K P R I S Y P A S M E H F K S S L T H T V K S R D E P T P D Q C P
221 CATTGAAGGAAGCGAAGCGGACATCGACACCGTGGCGATATACCAACTTTTGGATTTTTCAGCCGAGCTGGTTCGCTACAAAGGAATTTGGGACAAGTCTTCGAGGAT
74 A L K E S E A D I D T V A I Y P T F D F Q P S W L R T K E F W D K S F E D
331 CGGTATGAAAGAATTCTAACGACACTACCGGCTAGACTGAAGTAATCGTGGTCTCTCACTCACACAACGACCGGGATGGCTGAAGACGTTTGAACAGTACTTCGA
111 R Y E R I H N D T T R P R L K V I V P H S H N D P G W L K T F E Q Y F E
441 GTGGAACACCAAGAACATTATCAACACATAGTGAACAACTGCACCACTACCCCAACACTGACCTTCATTGGACCGAGATATGCTTTCTGAATGCTGGTGGGAAAGGT
147 W K T K N I I N N I V N K L H Q Y P N M T F I W T E I S F L N A W W E R
551 CGCACCTGTCAACAAAAGGCAATTGAAAAAATTTATCAAGAAGGTCTCTCGAGATCAGACGGGCGGCTGGGTGATCGCGGACGAAGCCTGCACGATATCTATGCG
184 S H P V K Q K A L K K L I K E G R L E I T T G G W V M P D E A C T H I Y A
661 CTAATTGACCAAGTTTATGAAGGACATCACTGGGTGAAACTTAATCTCGGCGTCACTCCGAGAGCAGGATGGTCTATTGACCCCTTCGGCCACGGGGCACTGTGCTTA
221 L I D Q F I E G H W V K T N L G V I P K T G W S I D P F G H G A T V P Y
771 CCGTACAGACGAGCGGCTTGAAGGAACATTATACAGAGAATCCATTATGCTGGAACAGTGGCTGGCGAGCGACAGATTGAGGAGTTTACTGCGTGGCGAGTT
257 L L D Q S G L E G T I I Q R I H Y A W K Q W L A E R Q I E E F Y W L A S
881 GGGCTACTACGAAGCGCTCCATGATAGTGCACATCAGCGTTTGAATTTATTTCAATAAAAAGCACGTTGGCGCCGACCCCTTCAATTTGCTCAGTTTTCGACTCAGG
294 W A T T K P S M I V H N Q P F D I Y S I K S T C G P H P S I C L S F D F R
991 AAGATTCCCGCGCAATTTCTGAATACACAGCTAAGCAGAGACATCCGGAACACACTTGCACAGCAAGGCAAGACTTTGATAGAGGAGTACGACCTTACCGGTC
331 K I P G E Y S E Y T A K H E D I T E H N L H S K A K T L I E E Y D R I G S
1101 CCGTACTCCACCAAGCTGGTGTGCTGGTGGCGTGGGAGCAGTTCAGATACGACTACAGCGTTCGAGTTTGTATGCCAATACGTCAATATGTAATGTTTAACTACA
367 L T P H N V V L V L P L G D F R Y E Y S V E F D A Q Y V N Y M K M F N Y
1211 TCAATGCTCACAAGGAATCTTCAACGCTGACGTACAGTTCCGAACTCTCTCGATTACTTTAACGCCATGAAAGAAAGACATCAAAATATACCCAGCTTAAAGGGAGAT
404 I N A H K E I F N A D V Q F G T P L D Y F N A M K E R H Q N I P S L K G D
1321 TTCTTCTGTTTACTCCGATATTTTCAAGCAAGTAAACAGCGTACTGGTCAAGTTACTACTACTAGACCTTACCAAAAAATCTCGCCCGTCAAGTTCGAACACCAACT
441 F F V Y S D I F S E G K P A Y W S G Y Y T T R P Y Q K I L A R Q F E H Q L
1431 GCGATCGGAGAGATTTTATCCCTTGTATCGAATACATCAGACAGATGGGTGCCCAAGGAGAGTTCCGAGCTTCTGAGAAAAAGTTAGAAAAATCTTACGAGCAGC
477 R S A E I L F T L V S N Y I R Q M G R Q G E F G A S E K K L E K S Y E Q
1541 TTATCTATGCTCGACGGAATCTGGTCTGTTTCAACTCAGGATCGGATTACTGGAACTCAAAAGTCCAGTGTGATCGAAGATTACGGAACCAAACTGTTTCAAAAGTCTG
514 L I Y A R R N L G L F Q H H D A I T G T S K S S V M Q D Y G T K L F T S L
1651 TATCACTGCATCCGCTGCAGGAGGCGCGCTCACCACCATCATGTTGCTGACCACTGCTTGCCTGACGAGTTCGCTGACGAGCATTATACAAAGCGAGGTTGAGTGGGAACTTACGG
551 Y H C I R L Q E A A L T T I M L P D Q S L H S Q S I I Q S E V E W E T Y G
1761 AAAACGCCCAAGAGCTGCAACTGCTCTTCAAGCAAGAAAGTATTAATTTTAACTCCGTTGGCTGAGACTCGAAGTGGTTCAGGTTAGATCCAACTGCT
587 K P P K L Q V S F I D K K V I L F N P L A E T R T E V V T V R S N T
1871 CCAACATCCGGGTGATACGATACACAAAGAGGAGCAGCTTGTATCAGATAATGCCAGCATCAACATCCAAGACAACGGCAAGAGTATCGTAAGCGACACCACTTC
624 S N I R V Y D T H K R K H V L Y Q I M P S I T I Q D N G K S I V S D T T F
1981 GACATAATGTTTGGTGGCCACCATCCCGCCCTCACCCTCCATCTCGTACAAGTGCAGGAGCACACCAACTTCCCACTCGCTCATTTTCTGCAACAACTGCGAACA
661 D I M F V A T I P L T S I S Y K L Q E H T N T S H C H V I F C N N C E Q
2091 ATACCAGAAATCCAATGTTTCCAAATTAAGAAATGATGCTGCTGACATACAATAGAAATGCAAGTGTCTAACTTCTCGTTAATAGGAACACCGGCTTCTGAGAC
697 Y Q K S N V F Q I K K M M P G D I Q L E N A V L K L L V N R N T G F L R
2201 AAGTCTATAGAAAGGACATCCGGAAGAGAACTGCTGTTGACGTACAATTCCGGCGATATCAAAAGTGCCCAAGACATTCTGGTGTCTTACCTCTTCATGCTCTTATACGAC
734 Q V Y R K D I R K R T V V D V Q F G A Y Q S A Q R H S G A Y L F M P H Y D
2311 TCACCTGAGAAGAATGTTCTGCATCCCTACACTAATCAGAACAACATGCAAGATGATAACATAATCATAGTGTCCGGACCTATTTCTACGGAATCAGCAGCATGTACTT
771 S P E K N V L H P Y T N Q N N M Q D D N I I I V S G P I S T E I T T M Y L
2421 GCCCTTCTTGGTGCACACTATTAGGATATACAACTGCGGAGCCCGGTACTGCTGCTGCTATTCTATTAGAGACCGATGATAGATTTCGAGGCGCCACATAGAACAGAG
807 P F L V H T I R I Y N V P D P V L S R A I L L E T D V D F E A P P K N R
2531 AGACTGAGTTATTTATGACATTACAGCTGATATACAAAACGGTGACATTCGGAATTTTACACCGATCAGAACGGATTCCAGTACCAAAAGAGGGTCAAAGTGAATAAA
844 E T E L F M R L Q T D I Q N G D I P E F Y T D Q N G F Q Y Q K R V K V N K
2641 CTAGGAATAGAAGTAACTACTACCCGATCACTACCATGGCGTGCCTGCAAGACGAGGAGACCCGGTCACTCTGCTGACGAACCCGCTCAAGGCGCTGCTGCATACGA
881 L G I E A N Y P I T T M A C L Q D E T R L T L L T N H A Q G A A Y E
2751 ACCAGGACGCTTAGAAGTCATGCTCGATCCTCGAATCTTTATGATGACTTCAGAGGAATCGGTGAAGGAGTACTCGATAACAAACCGACGACTTCCAGAATCGATT
917 P G R L E V M L D R R T L Y D D F R G I G E G V V D N K P T T F Q N W I
2861 TAATTGAATCCATGCCAGGCGTGACGCGAGCCAAAGAGAGACACTAGTGAACAGGTTTCAAATTTGTTAATGAACGTCGTTTTGGCCCGGCGCAAGAGGAAGCCCTTAC
954 L I E S M P G V T R A K R D T S E P G F K F V N E R R F G P G Q K E S P Y
2971 CAAGTACCGTCCGAGACTACCTGAGCAGGATGTTCAATTAACCGGTGAACGTGTACCTGGTGGACACTAGCGAGGTTGGCGAGATCGAGGTGAAGCCGTACCA
991 Q V P S O T A D Y L S R M F N Y P V N V Y L V D T S E V G E I E V K P Y Q
3081 GTGCTTCTGTCAGAGCTTCCCGCCCGGATCCACCTGGTCACTCGGACCATCACCAGCAGGTCGCTCGAATCTTCCCAAGCAACGAAGCTACATGGTACTGCACC
1027 S F L Q S F P P G I H L V T L R T I T D D V L E L F P S N S Y M V L H
3191 GACCAGGATACAGCTCGGCTGTCGGAGAGAAGCCACTGCCAAGTCTCCCAAGTTTTCGTCCTCAAAACAGGTTCAATGGTCTGAACATTCAGAACATCACTGCACTGAGC
1064 P G Y S C A V G E K P V A K S P K F S S K T R F N G L N I Q N I T A V S
3301 CTGACCGGCTGAAGTCACTCCGACCTCTCAGGCTGAGTGACATCCACCTGAACGCTATGGAGTAAAACTTACAAGATCAGGTTTAA
1101 L T G L K S L R P L T G L S D I H L N A M E V K T Y K I R F
```

Human lysosomal mannosidase II (NM 000528)

1 ATGGGCTACGCGCGGGCTTCGGGGGCTTCGCGCTCGCGGCTGCCTGGACTCAGCAGGCCCTTGGACCATGTCCCGCGCCTCGCGGCACCGCTCCCGCCTCTCGCTTT  
10 M G Y A R A S G V C G V C A R G C L D S A G P W T M S R A L R P P L P L C F  
110 TCCTTTTGTCTGCGCGCTGCGCGTCTCGGGCGGGGATACGACAGTACGCCACAGCTCAGCGGAATCTGCGAACGTGCACCTGCTGCTCACACATGATGA  
37 F L L L L A A A G A G A R A G G Y E T C P T V Q P M N L N V H L L P H T H D D  
219 CGTGGGCTGCGTCAAAACGTGGACACGATCTTTATGAATCAAGAATGACATCAGCAGCGGGTGCAGTACATCTGGACCTGGTCATCTGCTCTGTGCGCA  
73 V G W L K T V D Q Y F Y G I K N D I Q H A G V Q Y I L D S V I S A L L A  
328 GATCCACCCGCTGCTTCATTACGTGGAGATTCGCTTCTTCTCCGTTGGTGGCACCAGCAGACAAATGCCACACAGGAAGTCGTGCGAGACCTTGTGCGCGAGGGG  
110 D P T R R F I Y V E I A F S R W H Q T N A T Q E V Y R D L V R Q G  
437 GCGTGGAGTTGCGCAATGGTGGCTGGGTGATGAACGATGAGGACGACCCACCATCGGTGGCCATCGTGGACAGAGTACATGGGCTGCGCTTTCTGGAGGACATT  
146 R L E F A N G G M N D E A T H Y G A I V D Q M T L G L R F L E D T  
546 TGGCAATGATGGGCGACCCGCTGTGGCTGGCAATTGACCCCTCGGCCACTCTCGGGAGAGGCTCGCTGTTTGGCAGATGGGCTCGACGGCTTCTTCTTGGG  
182 G N D G R P R V A W H I D P F G H S R E Q A S L F A Q M G F D G F F G  
655 CGCCTTGATTATCAAGATAAGTGGTACCGATCGAGAAGCTGGAGATGGAGCAGGTGTGGCGGGCGAGCACCAGCGCTGAAGCCCCCGACCGCGGACCTTCTACTGGTG  
219 R L D Y Q D K W V R M O K L E M E Q V W R A S T S L K P P T A D L F T G  
764 TGCCTCCAATGGTTACAACCGCCGAAGAATCTGTGCTGGATGTGCTGTGTCGATCAGCCGCTGGTGGAGGACCTCGCAGGCCCGAGTACAACCGCAAGGAGCT  
255 V L P N G Y N P P R N L K C W D V L C V D Q P L V E D P R S P E Y N A K E L  
873 GGTGATTACTTCTAAATGTGGCCACTGCCACGGCGCGTATACCGACCAACCACTGTGATGACCATGGGCTCGGACTTCCAATAGAAATGCCAACCATGTGG  
291 V D Y F L N V A T A Q G R Y R T N H T V M T M G S D F Q Y E N A N M W  
982 TTCAGAACCTTGACAGCTCATCCGGCTGGTAAATCGGCAGCAGGCAAAAGGAAGCAGTGTCCATGTTCTTACTCCACCCCGCTTGTACTCTGGGAGCTGAACA  
328 F K N L D K L I R L V N A Q A K G S S V H V L Y S T P A C Y L W E L N  
1091 AGGCCAACCTTCACTGGTCAGTGAACATGACGACTTCTTCCCTACCGGGATGGCGCCCCACGAGTTCTGGAACCGGTACTTTTCAAGTCGGCGCGGCTCAAAACGCTA  
364 K A N L T W S V K H D D F F Y A D G P H Q F W T G Y F S R P A L K R Y  
1200 CGAGCGCCTCAGCTACAACCTCTCGAGGTGTGCAACACAGCTGGAGCGCTGGTGGGCGTGGCGGCCAACGTGGGACCTATGGCTCGGAGACAGTGCACCCCTCAAT  
400 E R L S Y N F L Q V C N G L E A L V G L A N V G P Y G S D S A P L N  
1309 GAGGCGATGGCTGTGCTCCAGCATCAGCAGCGCTCAGCGGCACCTCCGCGCAGCATGGGCAAGCATCGCGGCCGAGCTTGGCGGAGGCTGGGGGCTTTCGAGG  
437 E A M A V L Q H G H D A V S G T S R Q H V A N D Y A R Q L A A G W G P C E  
1418 TCTCTTGAGCAACCGCTGCGCGGCTCAGAGGCTTCAAGATCACTTCACTTTTGCCAACAGCTAAACATCAGCATCTCGCCGCTCAGCCAGAGCGCGGCGCGCTT  
473 V L L S N A L A R L G F K D H F T F C Q Q L N I S I C P L S Q T A A R F  
1527 CCAGGTCATCGTTTATAATCCCTCGGCGGAAGTGAAATGGATACGGCTCCGCGTCAGCGAAGCGCTTTGTTGTGAAGGACCCCAATGGCAGGACAGTGGCC  
509 Q V I V Y N P L G R K V N W M V R L P V S E G V F V K D P N G R T V P  
1636 AGCGATCTGGTAAATTTTCCAGCTCAGACAGCGCGGCGGACCTCCGGAGCTGCTGTTTCTCAGCCTTACTCGCCCGCCTGGGCTTCAGCACCTTTCAGTGAAGCAGG  
546 S D V I F P S S D S Q A H P P E L L F S A S L P A L G F S T Y S V A Q  
1745 TGCCCTCGTGAAGCGCCAGCGCGCGCAGCAGCCATCCCCAGGAATCTGTGTCCTGCTTTAAACATCGAAATGAGCAGTCCGGGACAGGTTTGATCTGCTGA  
582 V P R W K P Q A R A P Q P I P R R S W S P A L T I E N E H I R A T F D P D  
1854 CACAGGGCTGTGTGAGAGATTAGAATGAATCAGCACTCTGCTGCTGTTTGGCGAGACCTTCTTCTGTTACAACCCAGTATAGGTGACAACGAAAGTGACCAG  
618 T G L L E I M N M N Q A L L L P V R Q T F F W Y N A S I G D N E S D  
1963 GCGTCAGGTGCTACATCTTCAGACCCAACCAAGAAACCGCTGCTGTGAGCGCTGGGCTCAGATCCACCTGGTGAAGACACCTTGGTGAGGAGGTGACCCAGA  
655 A S G A Y I F R P N Q K P L V S R W A Q I H L V K T P L V Q E V H Q  
2072 ACTTCTCAGCTTGGTGTCTCCAGGTGGTTGCGCTGTACCCAGGACAGCGGCACCTGGAGTCAAGTGGTGGTGGGCGGATACCTGTGGGCGACACTGGGGGGAAGA  
691 N F S A T A W C S Q V V R L Y P Q Q R H L E W S V G P I P V G D T W G K E  
2181 GGTCACTCAGCCGTTTTCACACACCGCTGGAGACAAAGGACGCTTACACAGACAGCAATGGCCGGGAGATCTGGAGAGGAGGCGGATTATCGACCCACTGGAAA  
727 V I S R F D T P L E T K G R F Y T D S N G R E I L E R R D Y R P T W K  
2290 CTGAACAGCAGGAGCCGCTGGCAGGAATCTATCCAGTCAACACCCGGAATTTACATCAGGATGAAATCGAGCTGACTGTGCTGACTGACCGCTCCGAGGGGG  
764 L N Q T E P V A G N Y P V N T R I Y I T D G N M O L T V L T D R S Q G  
2399 CGACGAGCTCAGAGATGGCTCGCTGGAGCTCATGGTGACCAAGGCTGCTGAAGGACGATGGACGGGATCTCGGAGCAGCAATAGGAGAACGGGTGGGGGGGTG  
800 G S S L R D G S G L E L M V H R R L K D D G R G V S E P L M E N S G A W  
2508 GGTGCGAGGGCCGACCTGGTGTGCTGGAACACAGCCAGGCTCGAGCGCGCGGACACCGGCTCCTGGCGGAGCAGGAGGTCTGGCCCTCAGGTGGTGTGCTGGCCCG  
836 V R G R H L V L L D T A Q A A A G H R L L A E Q E V L A P Q V L A P  
2617 GGTGGCGCGCGCTCAACTCTCGGGCTCTCCGCGCAGCAAGTCTCAGGCGTGGCAGGAGCTCGGCCCTCGGTGACACTGCTCAGCTGCGGACCTGGGGCC  
873 G G G A Y A Y C N L G A C P P R T Q F S G L R R D L P P S V H L L T L A S G  
2726 CCGAAATGGTGTCTGCTGCTGGAGCAGGTTTGGCTAGGAGAGGATTCGCGAGTAACTGAGCGCCCGGTTACCTTGAACCTGAGGGAGCTGTTTCTCACTT  
909 P E M V L L R L E H Q F A V G E D S G R N L S A P V T L N L R D L F S T F  
2835 CACCATACCCGCTCGAGGAGACACGCTGCTGGCCAAACGAGCTCCGCGAGGCGAGCTCCAGGCTCAAGTGGACACAAACACAGGCCACCCACCCCAACTCCG  
945 T I T R L Q E T T L V A N Q L R E A S S R L K W T T N T G P T P H Q T P  
2944 TACCAGCTGGACCGGCAACATCAGCTGGAACCCATGGAATCCGCACTTTCTGGCGCTCAGTCAATGGAAGAGGTTGGATGGTTAG  
982 Y O L D P A N I T L E P M E I R T F L A S V Q W K E V D G

Human cytoplasmic mannosidase II (NM\_006715)

1 ATGCGCGCAGCGCGCTTCTTGAAGCACTGGCGCACCACTTTTGAAGCGGGTGGAGAAGTTCTGTGCCCGATCTACTTCAACGACTGTAACTCCGCGGGCAGCGCTTTTGT  
2 1) M A A A P F L L K H W R T T T F R V E K F V S P I Y F T D C N L R G R L F  
110 GCGCCAGCTGCCCTGTGGCTGTGCTCTCCAGGTTCTTGACGCGGGAGAGCACTTCTTACGAGGAGGAGCTGACGCGGGGACTTCCGCGCGCGCAGCTCGGCGACAGCTT  
37) G A S C P V A L T G S S F L T P E R L P Y Q E A V O R D F R P A Q V G D S F  
219 CGGACCCACATAGGTGGACAGTCTGTGTTTCGGGTGGAGCTGACCATTCCAGAGGAGTGGGTGGCGCAGGAAGTTACCTTTGCTGGGAAGTGATGGAGAAGCTCGGTG  
73) G P T W W T C W F R V E L T I P E A W V Q E V H L C W E S D G E G L V  
328 TGCGCTGATGGAGAAGCTGTGCAGGGTTTAAACAAAGAGGGTGAGAAGACAGTATGTCTGACTGCAGGCTGGGGGAAAGAGACCCTCCGAAGCTCTACTCTCTATG  
110) W R D G E P V Q G L T K E G E K T S Y A V L T D R L G E R D P R S L T L Y  
437 TGGAAAGTACCTGCAATGGGCTCTGGGGCGGGAGGGAAGCATGATTGACAGCCCTCAGCTCAGAGAAGATTCCAGCTGAGCGCGGCTGAGCTAGCTGTGCTTCCA  
146) V E V A C A N G L L G A G K G S M I A A P D E K I F Q L S R A E L A V F H  
546 CCGGAGTGTCACATCTGCTCTGGTGGATCTGGAGCTGCTGCTGGGATCGCAACGAGGCTCTGGGAAGGACACACGAGCGAGCTTCCAGCGCTCTGACACCAATCA  
182) R D V H M L L V D L E L L L G I A K G L G K D N Q R S F Q A L Y T A N Q  
655 ATGGTGCAAGCTGTGTGACCTGCCAGCCGAGACCTTCCAGTGCCCGAGGCTGGCGCTCAGGTTCTTTGGCAACATGGGGGTGAAGCGCAACACCATTCATG  
219) M V N V C D P A Q P E T P F V A O A L A S R F F G Q H G G E S O H T I H  
764 CCACAGGGCACTGCCACATTGATACAGCTGGCTTTGGCCCTTCAAAGAGACTGTGAGGAAATGTGCCGGAGCTGGGTGACCGCCTGCAGCTCATGGAGCGGAACCC  
255) A T G H C H I D T A W L W P F K E T V R K C A R S W V T A L Q L M E R N P  
873 TGAGTTTCATCTTCCCTGCTCCAGGCGCAGCAGCTGGAATGGGTGAAGAGCTACCTTGKCGCTGACTCCGCACTCCAGGAGTTTGCCTGCTGGGACGTTTGTG  
291) E F I F A C S Q A Q Q L E W V K S R Y P G L Y S R I G Q E F A C R G O F V  
982 CCTGTGGGGGCACTGGGTGAAATGGATGGGAAGCTGCCAGTGGAGAGGCATGTTGAGGAGCTTTTTCGAGGGCAAGACTCTTTCTGAGGAGTTTGGGAAG  
328) P V G G T W V E M D G N L P S G E A M V R O F L Q G O N F F L Q E F G K  
1091 TGTGCTCTGAGTTTGGCTGCCGACACCTTTTGCTCTCAGCAGAGCTCCCCAGATCATGCAGCGCTGTGGCATCAGGCGCTTCTCACCAGAAATGAGCTGGAA  
364) M C S E F W L P D T F G Y S A Q L P Q I M H G C G I R R F L T Q K L S W N  
1200 TTTGGTGAACTCTTCCACACCAATCACTTTTGGGAGGGCTGGATGCTCCCTGCTACTGTCCTCCACTCCGCTCGGCACTCTATGGATCGAGGCGAGCGTG  
400) L V N S F P H T T F F W E G L D G S R V L V H F P P G D S Y G M Q Q S V  
1309 CAGGAGAGCTCTGAAGACCTGGCCCAACACGGGACAGGGCGGGCCCAACACAGTGCCTTCTCTTTGGCTTGGGATGGGGGTGTGGCCCAACCCAGACCATGC  
437) E E V L K T V A N N R D K G R A N H A S F L G F G D G G G C P T Q T M  
1418 TGGACCGCCTGAAGCGCCTGAGCAATACGGATGGGCTGCCAGGGTGAGCTATCTTCTCACAAGACAGCTCTTCTCAGCACTGGAGAGTGACTCAGAGCAGCTGTGCAC  
473) L D R L K R L S N T D G L P R A V C L S P R O L F S A L E S D S E O L C T  
1527 GTGGGTTGGGAGCTCTTCTGGAGCTGCACATATGCCATACACACCACTGCCAGATCAAGAAGGGGAACCGGGAATGTGAGCGGATCTGCAGCAGCTGGAGCTG  
509) W V G E L F L E L H N G T Y T H A Q I K K G N R E C E R I L H D V E L  
636) CTCAGTAGCTGGCCCTGGCCCGAGTGCCCACTTCTATACCCAGACCCGAGCTGCAGCACTCTGGAGGCTCTTCTTCTGAACCACTTCATGATGTGGTGACTG  
546) L S S L A L A R S A Q F L Y P A A Q L Q H L W R L L L L N Q F H D V V T  
1745 GAAGCTGCATCCAGATGGTGGCAGAGGAAGCCATGTGCCATTATGAAGACATCCGTTCCCATGGCAATACACTGCTCAGCGCTGCAGCCCGACCCCTGTGTGCTGGGA  
582) G S C I Q M V A E E A M C H Y E D I R S H G N T L S A A A A L C A G E  
1854 GCGAGCTCCTGAGGCGCTCTCATCTGCAACACACTGCCCTGGAAAGCGGATCGAAGTGAATGGCCCTCCCAAAACCGGGCGGGCCACACAGCTAGCCCTGTGTGACAGT  
618) P G P E G L L I V N T L P W K R I E A M A L P K P G G A H S L A L T V T V  
1963 CCGACAGTGGGCTATGCTCTGCTCTCTCCCAACCTCAGCTGCAGCCCTCTGCTGCCAGCGCTGTGTCTGATGCAAGAGACTGATGGCTCCGTGACTGTGACA  
655) P S M G Y A P V P P P T S L Q P L P Q Q P V F V Q E T D G S V L T D  
2072 ATGGCATCATCCGAGTGAAGCTGGACCCAACTGGTGCCTGACGTCTTGGTCTGGTGGCTCTGGCAGGAGGCCATTGCTGAGGCGCGCGTGGGGAACCACTTTGT  
691) N G I I R V K L D P T G R L T S L V L A S G R E A I E A G V N Q F V  
2181 GCTATTGTGATGATGTCCCTTGTATGGGATGCATGGGAGCTCATGAGTACCACTGGAGACAGGAAGCTGTGCTGGGCGAGGACGGACCTGGAGCTGGGACG  
727) L F D D V P L Y W D A W D V M D Y H L E T R K P V L G G A G T L A V G T  
2290 GAGGCGCGCTCGGGGACGCGCTGTGTTCTGTCTAGACATCAGCCCAAGCTGCCTGAGCAGAGGTTGTGCTGAGCTGTGGCTGCCCTATGTCCTGCTCCACA  
764) E G G L R G S A W F L L Q I S P N S R L S Q E V V L D V G C P Y V R F H  
2399 CCGAGGTACACTGGCATGAGGCCCCAAGTCTCTGAAGGTGGAGTTCCTGCTCGGCTGGGAGTTCCCAAGGCCACTATGAGATCCAGTTTGGGCACCTGCGAGCAC  
800) T E V H W H E A H K F L K V E F P A R V R S S Q A T Y E I Q F G H L R P  
2508 TACCACCTACAATACCTCTTGGGACTGGGCTGATTTGAGTGTGGGCGCCATCGGTGATGGATCTGTGAGAACAAGCGCTTTGGGCTGGCCCTGCTCAACGACTGCAAG  
836) T H Y N T S W D W A R F E V W A H R W M D L S E H G F G L A L L N D C K  
2617 ATGGCGCGCTGAGTGGAGGAGCAGCATCTCAGCCTCTCGCTCTCGGGCGCGCTAAAGCCCGGACGCTACTGTGACACGGGGCGCCACAGTTCACCTATGCACATGA  
873) Y G A S V R G S I L S L S L L R A P K A P D A T D T G R H E F T Y A L  
2726 TGCCGCACAAGGGCTCTTCCAGGATGCTGGCGTTATCCAAGCTGCCTACAGCTAAACTTCCCTGTGTGGCTGTGCCAGCCCCACCGCCGCGCCACCTCTGT  
909) M P H K G I T C C C A C C D A G V I Q A A Y S L N F P L L A P A P S P A T S W  
2835 GAGTGGCGTTTTCGGTGCTTCCAGCGCGTGTATGTGAGAGCTCTCAAGCAGGCGGAGAGCAGCCCGACCGCGCTCGCTGGTCTGAGGCTGATGAGGCGCCACCG  
945) S A F S V S S P A V V L E T V K Q A E S S P Q R R S L V L R L Y E A H G  
2944 AGCCACCTGGAGCTGCTGGCTGACTTGTGCTGCTGGGTTCAGGAGGCCATCTCTGCGATCTTGGAGCGACACAGACCTGCTGGCCACTGACTTGGGACCAACCGC  
982) S H V D C W L H L S L P V Q E A I L C D L L E R P D P A G H L T S G Q P  
3053 CTGAAGCTCACCTTTCTCCCTTCCAAGTGCTGCTGCTGCTGCTCAGCCTCCGCACTAGTCCCTGGGCTGGGTTTGTGTGAGAAGGCTCTGGG  
1018) P E A H L F S L P S A V P V T A R A S A S A T L S P W G G F V C R L R L W G  
3162 ACTCTCAATTTCTGCTTCCCAAGCCTAA  
1054) L L I S A S P A

